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(54) Live attenuated bacteria of the species Actinobacillus pleuropneumoniae

(57) The present invention relates to live attenuated bacteria of the genus *Actinobacillus pleuropneumoniae* that have a mutation in an *apxIV* gene such that no functional ApxIV toxin can be produced. The invention also relates to methods for the production of such bacteria. Also vaccines comprising such bacteria and methods for the production of such vaccines are part of the invention. The invention further relates to subunit vaccines comprising an ApxIV toxin, to methods for the production of such vaccines and to methods for the protection of animals against infection with bacteria of the genus *Actinobacillus pleuropneumoniae*. In addition, the invention relates to the promotor of the *apxIV* gene. Finally, the invention relates to diagnostic tests for the selective diagnosis of *Actinobacillus pleuropneumoniae* infections and to diagnostic tests discriminating between *Actinobacillus pleuropneumoniae* field strains and vaccine strains.

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Description

The present invention relates to live attenuated bacteria of the genus *Actinobacillus pleuropneumoniae,* having a mutation in a gene encoding a toxin, methods for the production of such bacteria, to vaccines comprising such bacteria, methods for the production of such vaccines, to vaccines comprising a toxin, methods for the production of such vaccines and methods for the protection of animals against infection with bacteria of the genus *Actinobacillus pleuropneumoniae.*

Bacteria belonging to the genus *Actinobacillus* all produce so-called RTX-toxins. (RTX stands for repeat in toxin).

It is the presence of these RTX-toxins that highly contributes to the pathogenic character of these bacteria.

The RTX-toxins have been extensively reviewed by Braun et al. (Critical Rev. in Microbiol. 18(2):115-158 (1991)). RTX-toxins in Gram-negative strains have also been reviewed in Welch, R.A. (Molecular Microbiology 5/3: 521-528 (1991)) and in Welch et al. (Inf. Agents and Disease 4: 254-272 (1995)).

All known RTX-toxins display some kind of cytotoxic or cytolytic activity. The target-cell-and host-specificity differ however, depending on the toxin and on differences in acylation (McWhinney et al.; J. Bact. 174: 291-297 (1992) and Hackett et al.; J. Biol. Chem. 270: 20250-20253 (1995)) . As a result of the difference in target cells, the various toxins of the RTX-toxin family are known e.g. as haemolysin, cytolysin or cytotoxin.

The genus *Actinobacillus* comprises a number of different species, inter alia, *Actinobacillus pleuropneumoniae, A. actinomycetemcomitans, A. suis, A. rossii, A. equuli and A. lig-nieresii.*

Actinobacillus pleuropneumoniae produces serotype-dependent RTX-toxins that are cytotoxic/cytolytic to pig, horse, bovine and human erythrocytes, to rabbit and porcine neutrophils and to porcine alveolar macrophages. (Rosendal et al; Am. J. Vet. Res. 49: 1053-1058 (1988), Maudsley J.R. and Kadis S; Can. J. Microbiol. 32: 801-805 (1986), Frey. J and Nicolet. J; Inf. & Imm. 56:2570-2575 (1988), Bendixon et al; Inf. & Imm. 33: 673-676 (1981), Kamp, E.M. and van Leengoed, L.A.M.G.; J. Clin. Microbiol. 27: 1187-1191 (1989)).

Infections with *Actinobacillus* in pigs are the cause of severe economic losses to pig industry, due to acute mortality in young pigs and reduced weight gain in older animals.

The genetic organisation of the operons involved in the synthesis, activation and transportation of the RTX toxins in Gram-negative bacteria has been reviewed recently by Coote, J.G. (FEMS Microbiology reviews 88: 137-162 (1992)). Frey has specifically reviewed the known three RTX-toxins in *Actinobacillus pleuropneumoniae* in Bacterial Protein Toxins, Zbl Bakt. Suppl. 24, p. 322-, Freer et al. (Eds.), Gustaf Fischer, Stutttgart, Jena, New York, 1994.

In *Actinobacillus pleuropneumoniae,* this kind of RTX-operon contains four genes: the actual Toxin-gene (A), an Activator-gene (C), and two genes (B and D) encoding proteins involved in secretion of the toxin into the surrounding medium. The primary translation-product of the Toxin-gene (A) is a non-toxic protein, of which the toxic activity is activated by the Activator-gene (C) product.

Until recently, it was assumed that only three RTX-toxins, all having the above-described genetic organisation or at least having the Toxin-gene (A) and Activator-gene (C) , existed in *Actinobacillus* species.

These three RTX-toxins, ApxI, Apx-II and Apx-III have respectively a pronounced haemolytic activity (ApxI), a mild haemolytic activity (Apx-II) or a macrophage-cytotoxic activity (Apx-III).

The various toxic activities are fairly randomly divided over the serotypes. There are four subgroups:

a subgroup A, represented by serotypes 1, 5, 9 and 11, producing ApxI and Apx-II,
a subgroup B, represented by serotypes 2, 3, 4, 6 and 8, producing Apx-II and Apx-III,
a subgroup C, represented by serotype 10, producing ApxI only,
a subgroup D, represented by serotype 7 and 12, producing Apx-II only,

It is known, that ApxI, -II, and -III all are essential elements in universal vaccines against *Actinobacillus pleuropneumoniae* infection: a vaccine not comprising at least ApxI, -II, and -III will not provide protection against all *Actinobacillus pleuropneumoniae* serotypes. Also, a vaccine not comprising at least the Apx-toxins of one specific serotype will not even induce protection against that single serotype.

Subunit vaccines based on in vitro synthesised RTX-toxins from *A. pleuropneumoniae* that lost their toxicity have been described earlier, e.g. in European Patent EP No. 0.354.628, in which subunit vaccines based upon a haemolysin and a cytotoxin of *A. pleuropneumoniae* are disclosed, and in European Patent EP No 0.453.024, in which *A. pleuropneumoniae* subunit vaccines based upon haemolysins, cytotoxins and outer membrane proteins are disclosed.

There are however four important disadvantages to subunit vaccines in general:

- high amounts of antigenic material are needed in order to adequately trigger the immune system.
- usually, only B-cell immunity is triggered.
- several protective antigens are only triggered *in vivo,* and therefore can not be present in subunit vaccines.
- a live pathogenic bacterium has many important immunogenic molecules, such as Outer Membrane Proteins and

capsular polysaccharides, all potentially important for protection and thus to be included in an efficient subunit vaccine.

Next to the obvious problems mentioned under points one and two, especially the fourth point makes it difficult to make an efficient subunit vaccine.
This is e.g. illustrated by the *A. pleuropneumoniae* subunit vaccine disclosed in European Patent EP No 0.453.024 mentioned above, in which four different subunits (three RTX-toxins and an outer membrane protein) are combined in one vaccine.

It is clear, that in order to overcome the disadvantages of subunit vaccines against *Pasteurellaceae*-infection, a live attenuated vaccine would be highly desirable.
A live attenuated vaccine has the following advantages:

it can be administered in low doses (it is self-replicating)
it closely mimics the natural/wild-type infection
it provides all the possible immunologically important antigens at the same time.

Nevertheless, in spite of the clear advantages, no live vaccines based on *Actinobacillus pleuropneumoniae* were commercially available prior to the present invention. The reason for this lies in the following paradox: as mentioned before, ApxI, -II, and -III all are essential elements of universal vaccines against *Actinobacillus pleuropneumoniae* infection. Live vaccines therefore have to produce these three RTX-toxins. These three RTX-toxins are however strong virulence factors in all *Actinobacillus* species (see e.g. Coote, J.G.; FEMS Microbiology reviews 88: 137-162 (1992), Tascon et al.; Mol. Microbiol. 14: 207-216 (1994)), Jansen et al.; Inf. & Imm. 63: 27-37 (1995)).
Deletion of the RTX-toxins in order to attenuate the virulence of live App strains is technically feasible, but this does not provide a solution for the dilemma: such RTX-negative strains would be useless as live attenuated vaccine strains since they do no longer induce immunity in the host against the haemolytic/cytotoxic activity of *Actinobacillus pleuropneumoniae* field strains.
Virulence factors that, although important in the induction of immunity, do play a less important role in building up immunity than ApxI, -II and -III, and thus can in principle be deleted are however currently not known.

It would thus be highly desirable to have a site on the genome of App that attributes to virulence and therefore leads to an attenuated App strain when modified, whereas at the same time it is, although useful in triggering immunity, dispensable from a vaccine point of view. No such sites are however currently known. Moreover, it would be highly desirable if such a site would be universally present in all App strains, instead of being restricted to certain serotypes. Such a site would then allow all different serotypes to be attenuated by deletion of that same site.

It is one of the objectives of the present invention to provide such an attenuation site, universally present in all *Actinobacillus pleuropneumoniae* strains regardless their serotype.

Recently, a new gene was found in a serotype 1 strain of *Actinobacillus pleuropneumoniae* (Thesis T.J. Anderson Nov. 1995).
Although this gene does not resemble the known *Actinobacillus* ApxI, -II and -III genes, it bears resemblance to RTX-toxin genes known from bacteria belonging to *Neisseria meningitidis,* for which reason it was named RTX-gene *apxIV.* The gene however differs in almost all aspects from the three known RTX-toxin genes *apxI, -II* and -III present in the various species of the *Actinobacillus* family as described above. First of all, the genomic organisation is completely different. Secondly, there is no activator-mechanism as is found for the known Apx-toxins. In the third place, no specific *in vivo* haemolytic or cytotoxic activity could at that time be attributed to the gene, or it's possible gene product.
It was now surprisingly found that this gene, fully in contrast with the three known RTX-genes, is present in all bacteria of the species *Actinobacillus pleuropneumoniae,* regardless their serotype. This was determined by hybridisation of a probe comprising apxIV coding sequences with restriction fragments of the DNA from *Actinobacillus pleuropneumoniae* of all serotypes as described in Example 6 and 7.
Unexpectedly it was found now, that *apxIV* deletion mutants are viable, but they behave less virulent compared to their apxIV-possessing parent strains.
Therefore, it was determined that the gene product, the ApxIV toxin is a virulence factor in all *Actinobacillus pleuropneumoniae* strains. This is an unexpected conclusion, since up until now, no effects at al, let alone effects possibly influencing virulence had been attributed to the gene product *in vivo.* In fact, up until now there was not even proof that the gene was expressed in *Actinobacillus pleuropneumoniae in vivo* or *in vitro* anyway.
It therefore is one of the merits of the invention that it was found that:

- the *apxIV* gene is present in all *A. pleuropneumoniae* strains regardless the serotype,
- the *apxIV* gene product is a virulence factor in all *A. pleuropneumoniae* serotypes,
- *A. pleuropneumoniae* strains with a deletion in the *apxIV* gene are still viable but have a decreased virulence

without significantly impairing the immunogenic properties of the strains,

Therefore, the invention provides for the first time live attenuated bacteria of the species *Actinobacillus pleuropneumoniae,* that do not produce a functional ApxIV toxin.

A functional ApxIV toxin is considered to be a protein that has all the characteristics of the ApxIV toxin as expressed in a wild-type bacterium, and is expressed at the wild-type level. Therefore, a non-functional ApxIV toxin is considered to be a toxin that lacks some or all of the characteristics of the ApxIV toxin as expressed in a wild-type bacterium, and/or is expressed at a level, insufficient to obtain wild-type effects of ApxIV toxin.

The inability to produce the ApxIV toxin can e.g. be due to modifications in the coding sequence encoding the ApxIV toxin. It may also be e.g. the result of modifications in regions known to be involved in transcription of the *apxIV* gene, such as the promotor region, or of modifications in regions involved in translation, such as the ribosome binding site.

The overall structure of the *apxIV* gene is given in figure 1.

In this figure, the direct repeat regions, characteristic for ApxIV toxin are indicated by dashed boxes, whereas the also ApxIV-specific glycine-rich nonapeptide regions are indicated by black arrows. The repeats are found at the C-terminal part of ApxIV. These characteristic features are present in all *Actinobacillus pleuropneumoniae* serotypes. The nucleic acid sequence and amino acid sequence of two serotypes are represented in SEQ. ID. No. 1-4. SEQ. ID. NO. 1 shows the nucleic acid sequence of the *apxIV* gene of App serotype 1, and SEQ. ID. NO. 2 shows the matching amino acid sequence of the serotype 1 ApxIV toxin. SEQ. ID. NO. 3 shows the nucleotide sequence of the *apxIV* gene of App serotype 3, whereas SEQ. ID. NO. 4 shows the matching amino acid sequence of the serotype 3 ApxIV toxin. Figure 2 shows the strikingly high level of conservation at amino acid level, especially in the N-terminal 650 amino acids, between the Apx-toxins of the various *Actinobacillus pleuropneumoniae* serotypes. This is also a remarkable characteristic of the *apxIV* genes. It is clear from figure 1, that a variation in the number of repeats at the C-terminal part of the toxin may occur, depending on the serotype. This variation accounts for the difference in size of the genes and encoded toxins obtained from the various serotypes.

There may be some variation in nucleic acid sequence even between *apxIV* genes isolated from different isolates of *Actinobacillus pleuropneumoniae,* belonging to the same serotype. This is due to natural variation well known in the art to exist in all organisms. It is possible that some amino acids in the ApxIV toxin encoded by the *apxIV* gene are replaced by others in the ApxIV toxin of another serotype, while the polypeptide is not altered in its function. For instance, a polypeptide containing Asp at a certain site, and its variant containing Asn at the comparable site still have the same properties. This process in which an amino acid is replaced by an functionally analogous amino-acid is called functional displacement. In this case the variant proteins are called functional variants. Another cause of variation is the phenomenon of degeneracy of the genetic code. Shortly, it means, that e.g. the amino acid glutamic acid is coded for by both GAT and GAA. This phenomenon holds for all amino acids, except Met and Trp. Thus, it is obvious, that e.g. the ApxIV toxin of serotype 1, as given in the present invention can not only be coded for by the nucleotide sequence given in SEQ ID NO: 1 but also by a very large variety of other sequences, still all giving the same or functionally the same polypeptides.

Therefore, a variant apxIV sequence encoding a polypeptide that is functionally comparable to the ApxIV toxin falls within the scope of the present invention.

Live attenuated bacteria according to the invention can be obtained in several ways. One possible way of obtaining such bacteria is by means of classical methods such as the treatment of wild-type *Actinobacillus pleuropneumoniae* bacteria with mutagenic agents such as base analogues, treatment with ultraviolet light or temperature treatment. Strains that do not produce a functional ApxIV toxin do not or to a lesser extend induce anti-ApxIV toxin antibodies, and therefore can easily be selected in animal tests. The necessary antiserum can be obtained as described below in Example 3.

Another possibility is to deliberately introduce, using recombinant DNA-technology, a well-defined mutation in the gene encoding the ApxIV toxin. Such a mutation may be an insertion, a deletion, a replacement of one nucleotide by another one or a combination thereof, with the only proviso that the mutated gene no longer encodes a functional ApxIV toxin. It can easily be seen, that especially mutations introducing a stop-codon in the open reading frame, or mutations causing a frame-shift in the open reading frame are very suitable to obtain a strain which no longer encodes a functional ApxIV toxin. Such mutations can e.g. be made by means of in vitro site directed mutagenesis using the Transformer® kit sold by Clontech. Many other standard recombinant DNA techniques such as digestion of the gene with a restriction enzyme, followed by endonuclease treatment and religation, are equally applicable.

Therefore, in a preferred form, this embodiment of the invention relates to live attenuated bacteria in which the gene encoding the ApxIV toxin comprises a mutation.

Well-defined mutations involving the deletion of fragments of the *apxIV* gene or even the whole gene, or the insertion of heterologous DNA-fragments, when compared to classically induced mutations, have the advantage that they will not revert to the wild-type situation.

Thus, in a more preferred form, this embodiment of the invention refers to live attenuated bacteria in which the gene encoding the ApxIV toxin comprises an insertion and/or a deletion.

Given the large amount of vaccines given nowadays to pigs, it is clear that combined administration of several vaccines would be desirable, if only for reasons of decreased vaccination costs. It is therefore very attractive to use live attenuated vaccine strains as a recombinant carrier for heterologous genes, encoding antigens selected from other pathogenic micro-organisms or viruses. Administration of such a recombinant carrier has the advantage that after administration of such a carrier, immunity is induced against two or more diseases at the same time. The live attenuated bacteria according to the present invention provide a very suitable carrier for heterologous genes, since the gene encoding the ApxIV toxin can be used as an insertion site for such heterologous genes. The use of the *apxIV* gene as an insertion site has the advantage that at the same time the *apxIV* gene is inactivated, and the newly introduced heterologous gene can be expressed in accordance with the homologous *Actinobacillus pleuropneumoniae* genes. The construction of such recombinant carriers can be done routinely, using standard molecular biology techniques such as homologous recombination. Therefore, in an even more preferred embodiment, the present invention relates to live attenuated bacteria of the species *Actinobacillus pleuropneumoniae* that do not produce a functional ApxIV toxin, and in which there is a heterologous gene inserted in the *apxIV* gene. Such a heterologous gene can, as mentioned above, e.g. be a gene encoding an antigen selected from other pathogenic micro-organisms or viruses. Another possibility is to insert a gene encoding a protein involved in triggering the immune system, such as an interleukine or an interferone.

In a still even more preferred form of the invention, the heterologous gene encodes one or more antigens selected from the group consisting of Porcine Reproductive Respiratory Syndrome (PRRS) virus, Pseudorabies virus, Porcine Influenza virus, Porcine Parvovirus, Transmissible Gastroenteritis virus, rotavirus, *Escherichia coli, Erysipelothrix rhusiopathiae, Pasteurella multocida, Bordetella bronchiseptica, Haemophilus parasuis* and *Streptococcus suis.*

There is however a serious pitfall in expression of heterologous genes in recombinant carriers: it is known that several proteins are toxic if they are expressed in heterologous bacteria. Therefore, genes encoding such proteins can never be introduced in heterologous carriers, since successful recombinants will eventually die as a result of the expression a certain amount of the heterologous gene. The P2-protein of *Haemophilus influenzae,* to name just one example, can simply not be expressed in *E. coli.* (Munson et al., Infect. & Immun. 57: 88-94 (1989)). It is one of the objectives of the present invention to offer a recombinant live carrier that does not have this drawback. It was unexpectedly found, that although the *apxIV* gene is efficiently expressed *in vivo (see Example 5),* it is not expressed *in vitro* (see Example 4). This was concluded from the failure to show the presence of ApxIV toxin in *in vitro* grown *A. pleuropneumoniae* cultures. This means that ApxIV expression is switched on or off, depending on the environment in which *A. pleuropneumoniae* is grown. This feature offers an unexpected advantage over known live recombinant carriers: if the expression of the heterologous gene is brought under the control of the *apxIV* promoter, the live attenuated P. pleuropneumoniae carrier according to the invention can be grown in vitro to high densities, regardless the inserted heterologous gene, since the foreign gene will not be expressed under these conditions. After administering a number of bacteria to the host, the expression of the heterologous gene will start and at some time during replication or after the death of the bacterium it will become available to the immune system of the host. The heterologous gene to be expressed can be functionally linked to the *apxIV* promoter by e.g. replacing the coding sequence of the apxIV gene by the coding region of the heterologous gene. It is not necessary to replace the whole *apxIV* gene: it suffices to replace the ATG-codon of ApxIV by the coding region of the heterologous gene including its stop-codon. It is also possible to express a heterologous gene under the influence of the *apxIV* promoter by making a fusion construct. This can be made by inserting the heterologous gene in frame with the *apxIV* reading frame downstream of the *apxIV* ATG codon.

The wording "functionally linked to the *apxIV* promoter" means that transcription of the heterologous gene starts at the apxIV promoter.

It goes without saying that each location of the inserted heterologous gene in which it is functionally linked to the *apxIV* promotor falls within the scope of the invention.

Therefore, the most preferred form of this embodiment relates to live attenuated bacteria according to the present invention, carrying a heterologous gene that is functionally linked to the promotor region of the *apxIV* gene.

The surprising finding that the native *apxIV* promotor is a switchable promotor that is switched off *in vitro* and switched on *in vivo* makes this promotor a very versatile expression tool both in it's natural host and as a heterologous promotor in other bacteria. When used as a heterologous promotor in other bacteria, the DNA comprising the promotor can be isolated from its host and transferred to a bacterium other than *Actinobacillus pleuropneumoniae.* Another option that has now become feasible, is the cloning of several copies of the *apxIV* promotor each controlling the expression of another gene. This can be done in the host bacterium *Actinobacillus pleuropneumoniae,* but this principle of multiple copies is equally applicable to other bacteria. As mentioned above, the promotor can be used for the selective *in vivo* expression of one or more heterologous genes encoding antigens selected from other pathogenic micro-organisms or viruses. The promotor can also be used for the expression of a heterologous DNA sequence encoding a

cytokine such as an interleukin, Tumor Necrosis Factor or an interferon. Several cytokines, e.g. interferons are known to play an important role as immune modulators. Thus it may be advantageous to express such genetic information under the control of the *apxIV* promotor. Therefore, another embodiment of the invention relates to a nucleotide sequence harbouring the promotor controling the expression of the *apxIV* gene.

The switchable promotor that in the native situation controls the expression of the *apxIV* gene, was now found to be located in the DNA fragment between position 451 and 1132 of SEQ ID NO: 5. It is clear, that those parts of this DNA fragment that are not essential promotor elements need not necessarily be present in the fragment. Thus, shorter fragments of this DNA fragment in which the promotor activity is retained, are equally suitable for the expression of heterologous genes. Therefore, a more preferred form of this embodiment relates to a nucleotide sequence comprising the DNA fragment from position 451 to 1132 of SEQ ID NO: 5 or a subfragment thereof still having promotor activity.

Bacterial promotors all share two consensus regions, the so-called -10 and the -35 region. Although the flanking sequence of these consensus regions may to a certain extend influence the efficiency of the promotor, it can be advantageous to use only that part of the promotor region that comprises the DNA fragment between -35 and the ATG codon. This DNA fragment is located between position 617 and position 641 of SEQ ID NO: 5. Therefore, in a more preferred form of this embodiment the invention relates to a nucleotide sequence comprising the DNA fragment from position 617 to 641 of SEQ ID NO: 5.

The present invention also relates to ApxIV toxin as a subunit vaccine component.

Subunit vaccines will most probably comprise the three known Apx-toxins. This was mentioned above. Since it was unexpectedly found, that the ApxIV toxin is however present in all *A. pleuropneumoniae* serotypes as mentioned above, it is a desirable additional component of subunit vaccines: neutralising antibodies raised against the ApxIV toxin provide protection against the ApxIV toxin produced by each and every *Actinobacillus pleuropneumoniae* strain, regardless the serotype. Therefore, another embodiment of the invention relates to subunit vaccines for the protection of animals against infection with a bacterium of the species *Actinobacillus pleuropneumoniae,* that comprise purified ApxIV toxin. The ApxIV toxin can be administered alone, or in combination with any or all of the toxins ApxI, -II and -III mentioned above and/or e.g. in combination with Outer Membrane Proteins (OMPs) of *Actinobacillus pleuropneumoniae.* Such vaccines can easily be prepared by admixing ApxIV toxin in an amount sufficient to induce an immune response, and a pharmaceutically acceptable carrier. Production of the ApxIV toxin is possible by introducing the *apxIV* gene in a suitable expression vector, expression of the gene and isolation of the toxin. Many versatile expression systems are known in the art, such as bacterial expression systems, baculovirus expression systems and mammalian cell expression systems. In Example 3 it is described how to obtain the ApxIV toxin by expression of the gene in E. coli.

Still another embodiment of the invention relates to live attenuated vaccines comprising live attenuated bacteria as described above for the protection of animals against infection with a bacterium of the species *Actinobacillus pleuropneumoniae.* Such vaccines can be obtained by admixing live attenuated bacteria with a pharmaceutically acceptable carrier. These vaccines comprise at least an immunogenically effective amount of the live attenuated producing bacterium according to the invention. Immunogenically effective means that the amount of live attenuated bacterium administered at the moment of vaccination is sufficient to induce in the host an effective immune response to virulent forms of the RTX-toxin producing bacterium. The useful dosage to be administered will vary depending on the age, weight and animal vaccinated, the mode of administration and the type of pathogen against which vaccination is sought. The vaccine may comprise any dose of bacteria, sufficient to evoke an immune response. Doses ranging between 10^3 and 10^{10} bacteria are e.g. very suitable doses.

The pharmaceutically acceptable carrier may be as simple as water, but it may e.g. also comprise culture fluid in which the bacteria were cultured. Another suitable carrier is e.g. a solution of physiological salt concentration. Other examples of pharmaceutically acceptable carriers or diluents useful in the present invention include stabilisers such as SPGA, carbohydrates (e.g. sorbitol, mannitol, starch, sucrose, glucose, dextran), proteins such as albumin or casein, protein containing agents such as bovine serum or skimmed milk and buffers (e.g. phosphate buffer).

Optionally, one or more compounds having adjuvant activity may be added to the vaccine. Adjuvantia are non-specific stimulators of the immune system. They enhance the immune response of the host to the invading pathogen. Examples of adjuvantia known in the art are Freunds Complete and Incomplete adjuvans, vitamin E, non-ionic block polymers, muramyldipeptides, ISCOMs (immune stimulating complexes, cf. for instance European Patent EP 109942), Saponins, mineral oil, vegetable oil, and Carbopol (a homopolymer). Adjuvantia, specially suitable for mucosal application are e.g. the E. coli heat-labile toxin (LT) or Cholera toxin (CT).
Other suitable adjuvants are for example aluminium hydroxide, phosphate or oxide, oil-emulsions (e.g. of Bayol F (R) or Marcol 52 (R), saponins or vitamin-E solubilisate.

Therefore, in a preferred form, the vaccines according to the present invention comprise an adjuvant.

For administration to animals, the vaccine according to the presentation can be given inter alia intranasally, intradermally, subcutaneously, by aerosol or intramuscularly.

There are several ways to store both subunits and live organisms. Storage in a refrigerator is e.g. a well-known method. Also often used is storage at -70°C in a buffer containing glycerol. Bacteria can also be kept in liquid nitrogen.

Freeze-drying is another way of conservation. Freeze-dried bacteria can be stored and kept viable for many years. Storage temperatures for freeze-dried bacteria may well be above zero degrees, without being detrimental to the viability. Freeze-drying is equally applicable for subunits.

Freeze-drying can be done according to all well-known standard freeze-drying procedures. Optional beneficial additives, such as e.g. skimmed milk, trehalose, gelatin or bovine serum albumin can be added in the freeze-drying process. Therefore, in a more preferred embodiment, the vaccine according to the present invention is in a freeze-dried form.

In an even more preferred form of this embodiment, the vaccine additionally comprises one or more antigens selected from other pathogenic micro-organisms or viruses. Such a vaccine can be obtained by adding one or more antigens selected from other pathogenic bacteria or viruses to the live attenuated bacterium according to the invention and a pharmaceutically acceptable carrier as described above.

Of course, it is possible to add not only one or more antigens, but also one or more of the whole pathogens as such, in an inactivated or live form.

It can alternatively be obtained by cloning the genetic information encoding one or more antigens selected from other pathogenic micro-organisms or viruses into the live attenuated bacterium, using known recombinant DNA technology as described above.

Such vaccines are of course less stressing for the animal to be vaccinated than separate vaccinations with each of the pathogens, both from a medical and a physical point of view.

In a still even more preferred form, these antigens are selected from the group consisting of Porcine Reproductive Respiratory Syndrome (PRRS) virus, Pseudo-rabies virus, Porcine Influenza virus, Porcine Parvovirus, Transmissible Gastroenteritis virus, rotavirus, *Escherichia coli, Erysipelothrix rhusiopathiae, Pasteurella multocida, Bordetella bronchiseptica, Haemophilus parasuis* and *Streptococcus suis.*

The invention also relates to methods for the preparation of a live attenuated bacterium of the species *Actinobacillus pleuropneumoniae* that is not capable of producing a functional ApxIV toxin. These method comprise the introduction of a mutation in the gene encoding the apxIV protein. Both classical mutation techniques, using mutagenic agents, and recombinant DNA techniques well-known in the art for insertion, replacement or deletion of genetic information from the apxIV gene are applicable.

In a preferred form, the above mentioned methods are used for the introduction of a deletion.

Methods for the preparation of a live attenuated vaccine according to the invention, that comprise admixing bacteria according to the invention with a pharmaceutically acceptable carrier are also part of the invention.

Also falling within the scope of the invention are methods for the preparation of a subunit vaccine. Such methods comprise the mixing of purified ApxIV toxin with a pharmaceutically acceptable carrier.

Another generally acknowledged problem in the field of vaccination with live vaccines is the following: the presence of antibodies against a certain pathogen in the serum of a host animal indicates that the host has been infected with the pathogen, either in a virulent or attenuated form. It is however impossible to discriminate between field-infected animals and animals vaccinated with a live vaccine strain. The live attenuated *Actinobacillus pleuropneumoniae* according to the present invention offers a solution to this problem as follows:

As described in Example 3, the *apxIV* gene of *Actinobacillus pleuropneumoniae* serotype 1 has been isolated and expressed in a heterologous host cell. This expression product was subjected to PAAGE-gelelectroforesis and then used for Western-blotting. The blots were incubated with convalescent serum obtained from a deliberately *Actinobacillus pleuropneumoniae*-infected pigs, and sera from field-strains. It was found, that the *apxIV* gene is expressed *in vivo* in all *Actinobacillus pleuropneumoniae* field strains tested. This implicates, that pigs infected with *Actinobacillus pleuropneumoniae* will always have antibodies against the strain with which they were infected, regardless the serotype of the infectious strain.

The live attenuated bacteria according to the present invention can, due to the deletion of the *apxIV* gene, no longer make ApxIV toxin. Therefore animals vaccinated with a live attenuated *Actinobacillus pleuropneumoniae* strain according to the invention will not have antibodies against ApxIV toxin in their serum.

In a comparative test, e.g. an ELISA test, such sera will therefore react with all immunogenic *Actinobacillus pleuropneumoniae*-proteins such as e.g. ApxI, II and/or III, but not with ApxIV. Sera from pigs infected with an *Actinobacillus pleuropneumoniae* field strain however will react with all immunogenic *Actinobacillus pleuropneumoniae*-proteins, including ApxIV. Therefore, the live attenuated *Actinobacillus pleuropneumoniae* according to the present invention turns out to be a very suitable marker vaccine, i.e. a vaccine strain that can be discriminated from a field strain.

A diagnostic test for the discrimination between vaccine strains and field strains can be a simple ELISA-test in which purified ApxIV toxin is coated to the wall of the wells of an ELISA-plate. Incubation with serum from pigs to be tested, followed by e.g. incubation with a labelled anti-pig antibody can then reveal the presence or absence of antibodies against ApxIV toxin.

Another example of a diagnostic test system is e.g. the incubation of a Western blot comprising purified ApxIV toxin with serum of pigs to be tested, followed by detection of specific anti-ApxIV antibodies.

Therefore, diagnostic test for the discrimination between sera from pigs infected with *Actinobacillus pleuropneumoniae*

field strains and from pigs vaccinated with a vaccine comprising live attenuated vaccine *Actinobacillus pleuropneumoniae* strains according to the invention, that comprise purified ApxIV toxin. also fall within the scope of the invention.

Still another problem seen in pig health care is the following: It is difficult to determine in a both quick and unambiguous manner if a pig is infected with *Actinobacillus pleuropneumoniae* or *A. suis,* or possibly a combination of both. Diagnostic tests for the specific detection of A. suis are currently not available. This is mainly due to the fact that A. pleuropneumoniae and A. suis share so many antigens. As an example may serve, that two highly antigenic Apx-toxins; ApxI and ApxII have highly conserved homologues in e.g. A. suis (Van Ostaayen et al., submitted for publication). The known RTX-genes, encoding the ApxI, -II and -III toxins or homologues are found in practically all members of the genus *Actinobacillus,* such as *A. pleuropneumoniae, A. suis, A. rossii* and *A. equuli.* Thus, it was initially assumed by the inventors, that the new RTX-toxin ApxIV would also be common to all members of the genus *Actinobacillus.*
It was however found after testing a the swine-pathogenic *Actinobacillus,* again surprisingly in contrast with the known three RTX-genes, that this novel RTX-gene *apxIV* is only present in the swine-pathogen *Actinobacillus pleuropneumoniae.* It is absent in all other common swine pathogenic *Actinobacillus* species, and therefore it is also absent in *Actinobacillus suis.* See Example 6 and 7.
Therefore, it was surprisingly noticed that the presence of antibodies against ApxIV in the serum of a pig is a quick and unambiguous proof that the pig has been infected with A. pleuropneumoniae, and not with A. suis or any other swine-pathogen *Actinobacillus* species.
Thus the present invention also provides a diagnostic test based on the presence or absence of antibodies against ApxIV, and therefore a discriminating test for specifically distinguishing an infection with *A. pleuropneumoniae* from an infection with *A. suis* Such a test can e.g. be an ELISA test that comprises in separate wells the ApxI and -II toxins, present in both *A. pleuropneumoniae* and *A. suis* and the purified ApxIV toxin. Serum from A. suis-infected animals will react only with the wells comprising the ApxI and -II whereas *A. pleuropneumoniae-infected* animals will also react with the well comprising the purified ApxIV toxin.

Example 1:

Cloning and analysis of the *apxIV* gene of A. pleuropneumoniae serotype 1.

Standard molecular biological procedures (plasmid DNA isolation, restriction digestion, agarose gel electrophoresis, Southern blotting, ligation, transformation, electroporation) were, unless stated otherwise, essentially performed as described in Sambrook et al. (Molecular Cloning, A Laboratory Manual, Cold Spring Harbor, N.Y., 1989) or Ausubel et al., (Current Protocols in Molecular Biology. John Wiley & Sons, N.Y., 1987). PCR was performed essentially as described in Innis et al., (PCR protocols, A guide to Methods and Applications, Academic Press Inc., San Diego, 1990). Chromosomal DNA isolation was performed according to Pitcher et al., (Lett. Appl. Microbiol., 8;151-156, 1989). The origin of all *A. pleuropneumoniae* reference strains (serotype 1 : strain 4074; serotype 2: strain S1536: serotype 3: S1421; serotype 4 M62; serotype 5a: K17; serotype 5b: L20; serotype 6: femØ; serotype 7: WF83; serotype 8: 405; serotype 9: CVI13261; serotype 10: 13039; serotype 11: 56153 and serotype 12: 8329) is described by Frey and Nicolet, (J. Clin. Microbiol., 28;232-236, 1990). *A. pleuropneumoniae* serotype 3 strain HV114 is a field isolate (i.e. one of the serotype 3 strains tested in Beck et al., J. Clin. Microbiol., 32;2749-2754, 1994). Other *Actinobacillus* strains used; *A. rossii:* ATCC 27072; *A. equuli:* ATCC 19392; *A. suis:* ATCC 15558. *Pasteurella haemolytica* type 1 strain ATCC 14003 was used.
E. coli host strains used: XL1-blue (Stratagene, La Yolla, Ca; genotype: *recA 1 endA 1 gyrA96 thi- 1 hsdR17 supE44 relA 1 lac* [F' *proAB lacI^q ZDM15* Tn10 (Tet^r)]) and HMS174(DE3) (AMS Biotechnology Ltd, Switzerland; genotype: F$^-$ *recA* (r_{K12-} m_{K12+}) rif^r IDE3).
On the basis of the preliminary sequence data obtained from the thesis of T.J. Anderson (University of Guelph, 1995), two primers, designated APXIVA-1L (5'-TGGCACTGACGGTGATGA-3') and APXIVA-1R (5'-GGCCATCGACTCAACCAT-3'), were synthesised. These primers were used in a PCR amplification, with chromosomal DNA from *A. pleuropneumoniae* serotype 3 strain HV114 and serotype 1 reference strain 4074 as a template. With both strains a fragment of 442 bp was amplified. The fragment derived from the serotype 3 chromosomal DNA was labelled with Digoxigenin-11-dUTP (Boehringer Mannheim) according to the protocol of the manufacturer (this fragment was designated probe APXIVA, see fig. 4). The labelled probe was subsequently used to hybridize a Southern blot containing *ClaI* digested chromosomal DNA from strain 4074. The probe hybridised with a fragment of approximately 8.0 kb. The *apxIV* gene from serotype 1 strain 4074 was isolated by ligating *ClaI* digested chromosomal DNA into *ClaI* digested pBluescript II SK$^-$ (Stratagene USA). *E. coli* strain XL1-blue was transformed with the ligated DNA and transformants were selected on an LB plate with 100 mg/ml of ampicillin. Clones harbouring the *apxIV* were selected by colony hybridisation of a nitrocellulose replica of the plate with the APXIVA probe. Thus, a plasmid designated pROK7 was isolated and shown to harbour a *ClaI* insert of approximately 8 kb. The first 6736 bp of the *ClaI* insert were sequenced (SEQID 1) and an open reading frame of 4971 nucleotides was identified encoding a protein of 1657 amino acid residues (SEQID 2) with

a predicted size of approximately 186 kD. The gene was designated *apxIV_ var1* (see fig. 3).

Example 2:

Cloning and analysis of the *apxIV* gene of A. pleuropneumoniae serotype 3.

The labelled probe APXIVA (mentioned in example 1) was used to hybridize a Southern blot containing *Cla*I digested chromosomal DNA from strain HV114. The probe hybridised with a fragment of approximately 7.0 kb. The isolated chromosomal DNA from HV114 was digested with *Cla*I, and ligated with *Cla*I digested pBluescript II SK⁻(Stratagene USA). *E. coli* strain XL1-blue was transformed with the ligated DNA and transformants were selected on an LB plate with 100 mg/ml of ampicillin. Clones harbouring the *apxIV* were selected by colony hybridisation of a nitrocellulose replica of the plate with the APXIVA probe. Thus, a plasmid designated pROK5 was isolated and shown to harbour a *Cla*I insert of approximately 7 kb. The insert was analysed by sequence analysis (SEQID 3). An open reading frame of 4146 bp was identified encoding a protein of 1382 amino acid residues (SEQID 4), with a predicted size of approximately 154 kD. The gene was designated *apxIV_var3 (see* fig. 3) .

Example 3:

EXPRESSION OF ApxIV var3-polyhistidine fusion proteins in *E. coli*

From plasmid pROK5, a deletion clone was made which contains the 3' end of the *apxIV* gene, starting at the *Bam*HI site (nucleotide No. 2747 in SEQ ID No: 3) up to the *Cla*I site at the end of the insert downstream of the *apxIV* gene. This plasmid was designated pROK1. Using oligonucleotides APXIVAHIS1-L (5'-AGCCATATGGGCGAnTAAAnTCAG-3') and APXIVAHIS1-R (5'-TATGGATCCTCCGTGCTTCTGAGC-3') and DNA from plasmid pROK1 as a template, a DNA fragment of 2.1 kb was amplified (see fig. 4) containing the region from bp 3520 to 5643 in *apxIV_ var3* (SEQID 3) flanked with *Nde*I and *Bam*HI restriction sites at the 5' and 3' end respectively. After cloning of the *NdeI/Bam*HI digested PCR fragment in expression vector pETHIS-1, digested with the same enzymes, a plasmid designated pJFFapxIV6/10his-1 was obtained. Plasmid pETHIS-1 is a derivative of pET14b (Novagen Inc., Madison, Wi.) where the multiple cloning site has been extended and a region encoding a histidine decamer has been inserted. Consequently, The pJFFapxIV6/10his-1 plasmid contains a translational fusion encoding a histidine hexamer, followed by amino acid residues 653 up to 1360 from SEQID 4, followed by a histidine decamer, under the control of a T7 promoter. The plasmid was transferred to *E. coli* strain HMS174(DE3) with pLysS, which contains an IPTG inducible T7 RNA polymerase gene as well as the T7 lysozyme gene for increased stability. The strain was grown in LB medium containing 25 mg/ml of chloramphenicol and 100 mg/ml of ampicillin, up to an OD_{650} of 0.5, and induced with isopropyl-b-D-thiogalactopyranoside at a concentration of 10 mM. After the addition of IPTG, the cells were incubated at 37°C for 2.5 hours, the cells were harvested by centrifugation, and fusion protein with the expected size of 80 kD was isolated in the form of inclusion bodies. The inclusion bodies were solubilized in a solution of 6M guanidine hydrochloride, 300 mM NaCl and 50 mM NaH_2PO_4 at pH 8.0 and the 80 kD fusion protein was further purified by Immobilised Metal Affinity Chromatography (IMAC) (Schmitt et al., Molecular Biology Reports 18;223-230, 1993) using Ni^{2+} chelated columns (Qiagen AG, Basel). Pure protein was eluted from the column at pH 5.0. Pooled fractions were dialysed against a solution of 300 mM NaCl and 50 mM NaH_2PO_4 at pH 8.0. A rabbit was immunised with 500 mg of the polyhistidine fusion product, mixed with 1 volume of Complete Freunds Adjuvant (Difco Labs, Detroit, MI). A booster dose of the same amount, mixed with incomplete Fre-und Adjuvant was given 3 weeks later. Four weeks after the booster, the rabbit was bled and a hyperimmune serum comprising anti-ApxIV toxin antibodies , designated serum 522-409, was obtained.

Example 4:

Expression of apxIV genes in *in vitro* grown *A. pleuropneumoniae*

The *A. pleuropneumoniae* reference strain from serotype 1 was grown in Columbia broth supplemented with 10 mg/ml of b-NAD and harvested as described (Beck et al., J. Clin. Microbiol., 32;2749-2754, 1994). Adjacent to lanes comprising ApxIA, ApxIIA and ApxIVA-polyhistidine fusion proteins the concentrated culture supernatant was separated by polyacrylamide gel electrophoresis (Laemmli, Nature 227:680-685, 1970) and subjected to a Western blotting procedure (Towbin et al., Proc. Natl. Acad. Sci. USA 76:4350-4354, 1979). The Western blot was reacted with anti-ApxIA- and anti-ApxIIA monoclonal antibodies as described by Beck et al., (J. Clin. Microbiol., 32;27492754, 1994), and with anti-ApxIV serum 522-409 (see example 3). The isolated RTX toxin fraction of serotype 1 clearly contains ApxIA and ApxIIA. The presence of ApxIVA could not be demonstrated (see fig. 5).

Example 5:

Expression of apxIV genes in *A. pleuropneumoniae in vivo* during infection

A polyacrylamide gel containing the 80 kD polyhistidine-ApxIV_var3 fusion protein (see example 3) was transferred to a nitrocellulose membrane. The membrane was divided into strips which were reacted with (100-fold dilutions of) convalescent field sera against sero-type 1 or sera from a pig, expenmentally infected with the serotype 1 reference strain (Frey and Nicolet, Vet. Microbiol., 28;61-73, 1991). The reaction was visualised using alkaline phosphatase-labelled conjugate against rabbit IgG (Kirkegaard Perry Inc., Gaithersburg, Md.) and NBT (4-Nitrobluetetrazolium chloride) and BCIP (5-Bromo-4-chloro-3-indolyl-phosphate) colour development (see fig. 6). The serotype 1 field sera, as well as serum from the experimentally infected pig react with the 80 kD polyhistidine-ApxIV_var3 protein. This indicates that the ApxIV protein actually is expressed, is antigenic and induces anti-ApxIV toxin antibodies during *A. pleuropneumoniae* infection in pigs.

Example 6:

Presence of *apxIV* genes in all *A. pleuropneumoniae* serotypes and the absence thereof in non-*pleuropneumoniae Actinobacillus*-strains using Southern blotting

To investigate the presence of the *apxIV* gene in the various *A.pleuropneumoniae* serotypes and related bacteria, three probes were made (see fig. 4). Probe APXIVA is described in example 1. Probe APXIVA2 contains the 2015 bp DNA fragment between the *Bam*HI and *Nru*I sites. The 758 bp probe APPIVA1 was made by PCR amplification with oligos APPIV1-L (5'-GGGACAGTGGCTCAATTAAG-3') and (APPIV1-R (5'-AGCTGTAAACTCCACCAACG-3'). All probes were labelled with Digoxigenin-11-dUTP (Boehringer Mannheim) according to the protocol of the manufacturer and hybridised with Southern blots containing *Cla*I digested chromosomal DNA of all *A. pleuropneumoniae* reference strains and the HV114 field strain, *Actinobacillus suis* (ATCC 15558), *Actinobacillus rossii* (ATCC 27072) and *Actinobacillus equuli* (ATCC 19392). All three probes react similarly (see fig. 7 for the results with the APXIVA2 probe). All *A. pleuropneumoniae* strains react, whereas no hybridisation is observed with the *A. suis, A. equuli* and *A. rossii* strains.

Example 7:

Presence of *apxIV* genes in *A. pleuropneumoniae* and related strains using PCR amplification

With 50 ng of chromosomal DNA from the various *A. pleuropneumoniae* serotypes, other *Actinobacillus* species and *P. haemolytica* as templates, and primers APXIVA-1L (5'-TGGCACTGACGGTGATGA-3') and APXIVA-1R (5'-GGCCATCGACTCAACCAT-3') PCR amplification was performed. After analysis of the products on an agarose gel, products with the expected size of 442 bp were observed in all *A. pleuropneumoniae* amples, but in none of the other *Actinobacillus* species (fig. 8). This indicates that in addition to the results in example 6, also PCR could be used to discriminate *A. pleuropneumoniae* from other *Actinobacillus* species.

Example 8:

Overexpression of ApxIV-var1 polyhistidine fusion protein.

Starting with plasmid pROK-7 (see example 1) as a template and oligonucleotides APX4/II5-L (5'-CGCCATATGACAAAATTAACTATGCAAG) and APX4II6-R (5'-CGCGAAT TCAGCGACACAAGAGATAT) as PCR-primers, a PCR fragment was amplified. A sufficient amount of this fragment was then digested with restriction enzymes NdeI and EcoRI and cloned in expression vector pETHIS-1, digested with the same enzymes as described in Example 3. From the resulting plasmid, designated pJFFApxIVA1His1, a 206 kD polyhistidine fusion protein (MW determined in PAGE) of 1841 amino acid residues was overexpressed in E. coli as described in Example 3. The protein is encoded in the coding region spanning nucleic acid no. 1132 to 6546 as depicted in SEQ ID NO: 5. The amino acid sequence of the protein in given in SEQ ID NO: 6. In Western blot this product was shown to react with specific anti-ApxIV serum 522-409 (antiserum described in example 3).

Example 9:

Protection of mice by vaccination with ApxIV against APP challenge.

The 206 kD polyhistidine-ApxIV fusion protein as described in Example 8 and a comparable 108 kD polyhistidine-ApxIA-fusion protein, both derived from serotype 1 reference strain 4074 genomic material, were overexpressed as described in example 3. The cell pellet of induced E. coli cells was resuspended into PBS buffer (1 g. cell pellet in 6 ml buffer) and sonicated on ice for two times 45 seconds on ice for lysis of the cells. After centrifugation for 20 minutes at 22.000 x g at 4°C, the supernatant was discarded and the resulting pellet was washed with a solution of 3M urea (pH 6.3). The urea was removed after centrifugation for 20 minutes at 22.000 x g, and the resulting pellet was solubilized in 6M GuanidiniumHCl (pH 8.0). The protein samples were standardised by specific protein content after densitometry of PAGE gels. The samples were diluted with PBS and formulated with an oil adjuvant.

Three groups of 15 mice each, were intraperitoneally immunised with the ApxIV antigen (36.3 microgram), ApxIA antigen (36.3 microgram), or the adjuvant alone. The vaccines were administered in a volume of 0.4 ml. Twenty-four days after the first vaccination, each group of mice was split in two groups of 7 and 8 mice which were boosted with half the amount of antigen. The groups of 7 mice were boosted intraperitoneally in a volume of 0.2 ml and the groups of 8 mice were vaccinated intramuscularly with 0. 1 ml in each hind leg. Thirteen days after the booster, the mice were challenged intraperitoneally with 1.5 10^8 cfu of a virulent serotype 1 strain .

Example 10:

Poreforming capacity of ApxIV:

Freshly induced E. coli cells expressing ApxIV were used as the source of protein for testing poreformation in artificial lipid bilayers as described by Maier et al., Infect. Immun., 64; 4415-4423(1996). The methods used for black lipid bilayer experiments have been described previously (Benz et al.; Biochim. Biophys. Acta 511: 305-319 (1978)). Membranes were formed from a 1% solution of asolectin (soybean lecitin type IV-S from Sigma, St. Louis MO) in n-decane. Zero current membrane potentials were measured with a Keithley 610 C electrometer 5-10 min. after a 10-fold salt gradient was established across the membranes (Benz et al.; Biochim. Biophys. Acta 551: 238-247 (1979)). The presence of ApxIV resulted in a high frequency of pore formation in the presence of 0.5 % cholesterol, with an average single channel conductance (G) of 4 nS.
These results indicate that the ApxIV induces pores into artificial bilayers and is therefore toxic to eukaryotic cells and thus is a virulence factor for A. pleuropneumoniae.

Legend to the figures:

Figure 1: Comparison of ApxIVAvar1 and ApxIVAvar3 (var stands for serotype). Graphic representation of the different features found in the C-terminal end. Dashed boxes represent the direct repeat regions in ApxIVA. Bold vertical bars indicate the position of glycine rich nonapeptides, and DNA polymerase family B signatures are indicated by black triangles. The amino acid sequence YSDSANSKK represents the spacer sequence in the ApxIVAvar3 gene. The sequence segment of ApxIVAvar1 which is deleted in ApxIVAvar3 is also indicated in the figure.

figure 2: Alignment of the amino acid sequences of direct repeat 1 (A), direct repeat 2 (B) and direct repeat 3 (C) of ApxIVAvar1 and ApxIVAvar3. The copies of each of the direct repeats 1, 2 and 3 are labeled by letters to distinguish them for the sequence comparison. Variant residues are shown in bold letters.

Figure 3: Partial restriction maps of pBLac7 (Thesis of T.J. Anderson University of Guelph, 1995), pROK7 and pROK5. The different open reading frames (ORF's) are indicated by arrows. The interrupted arrow of *lacZ* in pROK7 indicates partial sequencing of the gene. Potential *rho*-independent transcription terminators are indicated (W). Potential transcription start sites are indicated by a triangle. Restriction sites: A= *Asp700;* B= *Bam*HI; C= *Cla*I; E= *Eco*RV; Ec= *Eco*RI; H= *Hin*dIII; N= *Nru*I; Nd= *Nde*I; Nh= *Nhe*I; P= *Pst*I; S= *Spe*I; Sm= *Sma*I.

Figure 4: Location of the various oligonucleotides and probes on the map of the *apxIVAvar3* gene.

Figure 5: Expression of ApxIV in *in vitro* cultivated serotype 1 reference strain 4074. Panel A was reacted with the anti-ApxIA monoclonal antibody, panel B with anti-ApxIIA monoclonal antibody and panel C was reacted with anti-ApxIVA serum 522-409. Lane 1 contains ApxIA-polyhistidine fusion protein, lane 2 contains ApxIIA-polyhistidine fusion protein, lane 3 contains strain 4074 concentrated culture supernatant, lane 4 contains ApxIVA polyhistidine fusion protein.

Figure 6: Immunoblot showing the reactivities of sera from pigs which were experimentally infected with the reference strain of serotype 1 (lane 1) or pig sera from serotype 1 field infections (lane 2-4) with the 80 kD polyhistidine-ApxIV fusion protein. As a positive control (+), serum 522-409 was used, as a negative control (-), polyclonal rabbit

serum against ApxI and ApxII (Frey et al., Infect. Immun., 57;2050-2056, 1989) was used as a 1000-fold dilution.

Figure 7: Southern blot of ClaI digested genomic DNA hybridised with probe APXIVA2. Lanes 1-13: *A. pleuropneumoniae* reference strains; 1: serotype 1; 2: serotype 2; 3: serotype 3; 4: serotype 4; 5: serotype 5a; 6: serotype 5b; 7: serotype 6; 8: serotype 7; 9: serotype 8; 10: serotype 9; 11: serotype 10; 12: serotype 11; 13: serotype 12; 14: HV114 field strain; 15: *A. suis* (ATCC 15558); 16: *A. rossii* (ATCC 27072); 17: *A. equuli* (ATCC 19392). Molecular size markers are indicated (in kilobasepairs) on the left.

Figure 8: PCR amplification of *apxIV* using primers APXIVA-1L and APXIVA-1 R. Lane assignments: lanes 1 to 13 contain the *A. pleuropneumoniae* reference strains from serotypes1, 2, 3, 4, 5a, 5b, 6, 7, 8, 9, 10, 11 and 12 respectively; lane 14: strain HV114; lane 15: *A. suis* ATCC 15558; lane 16: *A. rossii ATCC* 27072; lane 17: *A. equuli* ATCC 19392; lane 18: *A. lignieresii* ATCC 49236; lane 19: *P. haemolytica* type 1 ATCC 14003. Molecular size markers (in kilobasepairs) are indicated on the left.

Annex to the description

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:
(A) NAME: AKZO Nobel N.V.
(B) STREET: Velperweg 76
(C) CITY: Arnhem
(E) COUNTRY: The Netherlands
(F) POSTAL CODE (ZIP): 6824 BM

(ii) TITLE OF INVENTION: Live attenuated Actinobacillus pleuropneumoniae

(iii) NUMBER OF SEQUENCES: 4

(iv) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6736 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Actinobacillus pleuropneumoniae
(B) STRAIN: 4074 (serotype 1 reference strain)

(vii) IMMEDIATE SOURCE:
(B) CLONE: pROK7

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1576..6549
(D) OTHER INFORMATION:/codon_start= 1576
/function= "RTX toxin"
/product= "ApxIV_var1"
/gene= "apxIV_var1"
/number= 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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ACCGGTGCGG TGGTGGTAAC CACTCCGCAA GATATTGCGT TATTAGATGC GGTGAAAGGT 120

ATTTCAATGT TCCAAAAAGT GTCGGTACCG GTCTTAGGTA TCATTGAAAA TATGAGCGTA 180

CATATCTGCC AAAATTGCGG TCACCACGAA GATATTTTCG GCACCGGCGG TGCGGAGAAA 240

GTGGCGAAGA AATACGGTAC TAAAGTATTA GGACAAATGC CGTTGCATAT TCGCTTACGT 300

CAAGATTTGG ATGCCGGCAC ACCGACCGTC GTTGCGGCAC CGGAACACGA AACCAGCCGA 360

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GCCTATATTG AATTAGCGGC AAAAGTCGCT TCGGAATTAT ACTGGCAAGG TTCGGTTATC      420

CCGTCTGAAA TTATGATTCG TGAAGTAAAA TAAGTTTTAA TAACCACGAA AACACAAAGA      480

ACACAAGCGG TAGAATTTGC AGAAAAATTT GCAAATCCTA CCGCTTTTTT ATTAGTACGA      540

TTCGCTGTTG GACTGCTATT TGATTTGGTT TGTCAGGATA TTATGTTATT GTAATGAAAT      600

GTTAGTGAAT TATTTTTATT AATTTGAAAG GAAACAAAAT GAAAATAAAA AAACGTTACA      660

TTGCGCTGTT GGTCTTAGGT GTCGTTATCA GCTATGCCTG GTATCAAAAT TATCAATGGG      720

AACAGCTGAT GTTAAGCGGT TATTGTGAAA AGGACGGAAG TTATTTTGAT GATAGGCATA      780

CGAAGCAAGA ACTGATTGAT AGGGCAATTA ACTATATGCT GGAGCATCAA TCTAAAAAAA      840

CATACGATGC TTATACTGAT GAACCTTTAG AAATAAAACC ATATTTAACA ATAGAGGAAT      900

TTAAAAAACT CAATCCAAAT TGTTGTGAAA TTACCTCATG GCCAGCAGAT GCAGTTCCAC      960

AAGATTGGGA TGTTCGTGTG GAAGGTAAGG CATATAGGTA TGTAATCGTA AAATATTTAA     1020

GAACCTTAGC AAATAGAGAA CCTGAACGAT GGGAAACTAG TATTGTTTTT GATAATTGCG     1080

GCAATCCTAA AAGAGCAAGC TACTTATATT ATTTAAAGAG AGAAATTTAT TATGACAAAA     1140

TTAACTATGC AAGATGTGAC CAATTTATAT TTATATAAAA CGAAAACTCT ACCTAAAGAT     1200

AGATTGGATG ATTCACTTAT TTCTGAAATA GGAAAAGGAG ATGATGATAT TGATAGAAAA     1260

GAATTTATGG TGGGGCCGGG ACGTTTTGTG ACCGCTGATA ACTTTAGCGT TGTAAGAGAT     1320

TTTTTTAATG CTGGGAAATC ACGCATTATT GCGCCGCAAG TCCCGCCTAT TCGTTCACAG     1380

CAGGAAAAAA TCTTGGTCGG TTTAAAACCG GGCAAATATT CCAAAGCGCA GATATTGGAA     1440

ATGCTGGGTT ATACGAAAGG CGGAGAAGTG GTAAATGGCA TGTTTGCCGG TGAAGTCCAG     1500

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                  1               5                  10

GGC AAA CGC TAT ATT GAA AAC TTT GGT ATT GAA CCT CTT GGT AAG CAA       1659
Gly Lys Arg Tyr Ile Glu Asn Phe Gly Ile Glu Pro Leu Gly Lys Gln
        15                  20                  25

GAA GAT TTT GAT TTT GTC GGC GGC TTT TGG TCT AAC TTA GTG AAT CGT       1707
Glu Asp Phe Asp Phe Val Gly Gly Phe Trp Ser Asn Leu Val Asn Arg
    30                  35                  40

GGT TTG GAA AGT ATT ATC GAC CCA TCC GGT ATC GGT GGA ACG GTA AAC       1755
Gly Leu Glu Ser Ile Ile Asp Pro Ser Gly Ile Gly Gly Thr Val Asn
45                  50                  55                  60

CTT AAC TTT ACC GGC GAG GTG GAA ACC TAC ACG TTA GAC GAA ACA AGG       1803
Leu Asn Phe Thr Gly Glu Val Glu Thr Tyr Thr Leu Asp Glu Thr Arg
                65                  70                  75

TTT AAA GCG GAA GCG GCG AAG AAA AGC CAT TGG AGT TTA GTG AAT GCG       1851
Phe Lys Ala Glu Ala Ala Lys Lys Ser His Trp Ser Leu Val Asn Ala
            80                  85                  90

GCG AAA GTA TAC GGC GGT TTA GAC CAA ATT ATT AAA AAA CTA TGG GAC       1899
Ala Lys Val Tyr Gly Gly Leu Asp Gln Ile Ile Lys Lys Leu Trp Asp
        95                  100                 105
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AGT GGC TCA ATT AAG CAT TTA TAT CAA GAT AAA GAT ACG GGC AAA TTA      1947
Ser Gly Ser Ile Lys His Leu Tyr Gln Asp Lys Asp Thr Gly Lys Leu
    110                 115                 120

AAA CCG ATT ATT TAC GGC ACG GCC GGC AAC GAC AGT AAG ATT GAA GGC      1995
Lys Pro Ile Ile Tyr Gly Thr Ala Gly Asn Asp Ser Lys Ile Glu Gly
125                 130                 135                 140

ACT AAA ATC ACC CGT AGG ATT GCG GGT AAA GAA GTT ACG CTT GAT ATT      2043
Thr Lys Ile Thr Arg Arg Ile Ala Gly Lys Glu Val Thr Leu Asp Ile
                145                 150                 155

GCC AAT CAG AAA ATT GAA AAA GGC GTG TTA GAG AAA TTG GGG CTG TCT      2091
Ala Asn Gln Lys Ile Glu Lys Gly Val Leu Glu Lys Leu Gly Leu Ser
            160                 165                 170

GTT AGT GGT TCG GAT ATC ATT AAA TTG TTG TTT GGA GCA TTG ACT CCA      2139
Val Ser Gly Ser Asp Ile Ile Lys Leu Leu Phe Gly Ala Leu Thr Pro
        175                 180                 185

ACT TTA AAT AGA ATG TTG CTA TCA CAA CTT ATC CAG TCT TTT TCC GAT      2187
Thr Leu Asn Arg Met Leu Leu Ser Gln Leu Ile Gln Ser Phe Ser Asp
    190                 195                 200

AGC TTG GCT AAA CTT GAT AAT CCC TTA GCC CCT TAC ACT AAA AAT GGC      2235
Ser Leu Ala Lys Leu Asp Asn Pro Leu Ala Pro Tyr Thr Lys Asn Gly
205                 210                 215                 220

GTG GTT TAT GTC ACC GGC AAA GGG AAT GAT GTG CTT AAA GGA ACT GAA      2283
Val Val Tyr Val Thr Gly Lys Gly Asn Asp Val Leu Lys Gly Thr Glu
                225                 230                 235

CAT GAG GAT TTG TTT CTC GGT GGT GAG GGG AAT GAT ACT TAT TAT GCG      2331
His Glu Asp Leu Phe Leu Gly Gly Glu Gly Asn Asp Thr Tyr Tyr Ala
            240                 245                 250

AGA GTA GGC GAT ACA ATT GAA GAC GCC GAC GGC AAA GGT AAA GTC TAT      2379
Arg Val Gly Asp Thr Ile Glu Asp Ala Asp Gly Lys Gly Lys Val Tyr
        255                 260                 265

TTT GTG AGA GAA AAA GGG GTA CCT AAG GCG GAT CCT AAG CGG GTA GAG      2427
Phe Val Arg Glu Lys Gly Val Pro Lys Ala Asp Pro Lys Arg Val Glu
    270                 275                 280

TTT AGC GAG TAC ATA ACG AAA GAA GAA ATA AAA GAG GTT GAA AAG GGG      2475
Phe Ser Glu Tyr Ile Thr Lys Glu Glu Ile Lys Glu Val Glu Lys Gly
285                 290                 295                 300

TTA TTA ACT TAC GCA GTT TTA GAA AAT TAT AAT TGG GAA GAG AAA ACG      2523
Leu Leu Thr Tyr Ala Val Leu Glu Asn Tyr Asn Trp Glu Glu Lys Thr
                305                 310                 315

GCG ACT TTC GCT CAT GCG ACT ATG CTT AAT GAG CTT TTT ACT GAT TAT      2571
Ala Thr Phe Ala His Ala Thr Met Leu Asn Glu Leu Phe Thr Asp Tyr
            320                 325                 330

ACT AAT TAT CGT TAT GAA GTT AAA GGA CTA AAA TTG CCC GCC GTT AAA      2619
Thr Asn Tyr Arg Tyr Glu Val Lys Gly Leu Lys Leu Pro Ala Val Lys
        335                 340                 345

AAG TTA AAA AGT CCG TTG GTG GAG TTT ACA GCT GAT TTA TTA ACT GTT      2667
Lys Leu Lys Ser Pro Leu Val Glu Phe Thr Ala Asp Leu Leu Thr Val
    350                 355                 360

ACG CCT ATT GAC GAA AAC GGA AAA GCA CTT AGC GAA AAA AGT ATT ACG      2715
Thr Pro Ile Asp Glu Asn Gly Lys Ala Leu Ser Glu Lys Ser Ile Thr
365                 370                 375                 380
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GTT AAA AAT TTT AAA AAT GGT GAT TTA GGA ATA AGG TTG TTG GAT CCT      2763
Val Lys Asn Phe Lys Asn Gly Asp Leu Gly Ile Arg Leu Leu Asp Pro
                385                 390                 395

AAT AGC TAT TAT TAT TTC CTT GAA GGC CAA GAT ACG GGT TTT TAT GGT      2811
Asn Ser Tyr Tyr Tyr Phe Leu Glu Gly Gln Asp Thr Gly Phe Tyr Gly
            400                 405                 410

CCT GCT TTT TAT ATT GAA CGA AAA AAC GGT GGC GGC GCT AAA AAT AAC      2859
Pro Ala Phe Tyr Ile Glu Arg Lys Asn Gly Gly Gly Ala Lys Asn Asn
        415                 420                 425

TCG TCG GGA GCA GGA AAT AGC AAA GAT TGG GGC GGG AAC GGG CAT GGA      2907
Ser Ser Gly Ala Gly Asn Ser Lys Asp Trp Gly Gly Asn Gly His Gly
    430                 435                 440

AAT CAC CGA AAT AAT GCC TCC GAC CTG AAT AAA CCG GAC GGA AAT AAT      2955
Asn His Arg Asn Asn Ala Ser Asp Leu Asn Lys Pro Asp Gly Asn Asn
445                 450                 455                 460

GGG AAT AAC CAA AAT AAC GGA AGC AAT CAA GAT AAT CAT AGC GAT GTG      3003
Gly Asn Asn Gln Asn Asn Gly Ser Asn Gln Asp Asn His Ser Asp Val
                465                 470                 475

AAT GCG CCA AAT AAC CCG GGA CGT AAC TAT GAT ATT TAC GAT CCT TTA      3051
Asn Ala Pro Asn Asn Pro Gly Arg Asn Tyr Asp Ile Tyr Asp Pro Leu
            480                 485                 490

GCT TTA GAT TTA GAT GGA GAT GGG CTT GAA ACC GTG TCG ATG AAC GGG      3099
Ala Leu Asp Leu Asp Gly Asp Gly Leu Glu Thr Val Ser Met Asn Gly
        495                 500                 505

CGA CAA GGC GCG TTA TTC GAT CAT GAA GGA AAA GGT ATT CGT ACC GCA      3147
Arg Gln Gly Ala Leu Phe Asp His Glu Gly Lys Gly Ile Arg Thr Ala
    510                 515                 520

ACG GGC TGG CTC GCT GCG GAT GAC GGT TTT TTA GTG TTA GAT CGT AAC      3195
Thr Gly Trp Leu Ala Ala Asp Asp Gly Phe Leu Val Leu Asp Arg Asn
525                 530                 535                 540

CAA GAC GGC ATT ATT AAT GAT ATA AGC GAG TTA TTT AGT AAT AAA AAT      3243
Gln Asp Gly Ile Ile Asn Asp Ile Ser Glu Leu Phe Ser Asn Lys Asn
                545                 550                 555

CAA CTT TCC GAC GGC AGT ATT TCT GCA CAC GGT TTT GCG ACA TTA GCC      3291
Gln Leu Ser Asp Gly Ser Ile Ser Ala His Gly Phe Ala Thr Leu Ala
            560                 565                 570

GAT TTG GAT ACA AAC CAA GAT CAG CGT ATC GAC CAA AAT GAT AAG CTG      3339
Asp Leu Asp Thr Asn Gln Asp Gln Arg Ile Asp Gln Asn Asp Lys Leu
        575                 580                 585

TTT TCT AAA CTC CAA ATT TGG CGG GAT TTA AAT CAA AAC GGT TTT AGT      3387
Phe Ser Lys Leu Gln Ile Trp Arg Asp Leu Asn Gln Asn Gly Phe Ser
    590                 595                 600

GAA GCG AAT GAG CTG TTT AGC TTA GAA AGT TTG AAT ATT AAA TCT TTA      3435
Glu Ala Asn Glu Leu Phe Ser Leu Glu Ser Leu Asn Ile Lys Ser Leu
605                 610                 615                 620

CAT ACC GCC TAT GAA GAG CGT AAT GAT TTT CTA GCG GGC AAT AAT ATC      3483
His Thr Ala Tyr Glu Glu Arg Asn Asp Phe Leu Ala Gly Asn Asn Ile
                625                 630                 635

CTT GCT CAG CTT GGG AAG TAT GAA AAA ACG GAC GGT ACT TTT GCA CAA      3531
Leu Ala Gln Leu Gly Lys Tyr Glu Lys Thr Asp Gly Thr Phe Ala Gln
            640                 645                 650
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ATG GGC GAT TTA AAT TTC AGT TTT AAC CCG TTT TAT AGC CGA TTT ACC      3579
Met Gly Asp Leu Asn Phe Ser Phe Asn Pro Phe Tyr Ser Arg Phe Thr
        655                 660                 665

GAA GCG TTA AAT TTA ACC GAG CAA CAA CGT CGC ACA ATT AAT CTA ACC      3627
Glu Ala Leu Asn Leu Thr Glu Gln Gln Arg Arg Thr Ile Asn Leu Thr
    670                 675                 680

GGC ACC GGT CGG GTT CGG GAT TTG CGT GAA GCC GCC GCA CTT TCT GAG      3675
Gly Thr Gly Arg Val Arg Asp Leu Arg Glu Ala Ala Ala Leu Ser Glu
685                 690                 695                 700

GAG TTG GCT GCT TTA TTA CAA CAG TAC ACT AAG GCC TCC GAT TTT CAG      3723
Glu Leu Ala Ala Leu Leu Gln Gln Tyr Thr Lys Ala Ser Asp Phe Gln
                705                 710                 715

GCA CAA CGA GAA TTA TTG CCT GCC ATT TTA GAT AAA TGG GCG GCA ACG      3771
Ala Gln Arg Glu Leu Leu Pro Ala Ile Leu Asp Lys Trp Ala Ala Thr
            720                 725                 730

GAT TTA CAG TAT CAA CAT TAT GAT AAA ACA TTA CTT AAA ACG GTA GAA      3819
Asp Leu Gln Tyr Gln His Tyr Asp Lys Thr Leu Leu Lys Thr Val Glu
        735                 740                 745

AGT ACC GAT AGT AGT GCT TCT GTC GTT AGA GTC ACG CCT TCT CAA TTA      3867
Ser Thr Asp Ser Ser Ala Ser Val Val Arg Val Thr Pro Ser Gln Leu
    750                 755                 760

AGT AGT ATA CGC AAT GCA AAG CAT GAT CCT ACC GTT ATG CAA AAC TTT      3915
Ser Ser Ile Arg Asn Ala Lys His Asp Pro Thr Val Met Gln Asn Phe
765                 770                 775                 780

GAA CAG AGT AAG GCA AAA ATT GCG ACT TTA AAT TCG CTC TAC GGG TTA      3963
Glu Gln Ser Lys Ala Lys Ile Ala Thr Leu Asn Ser Leu Tyr Gly Leu
                785                 790                 795

AAT ATC GAT CAA CTT TAT TAC ACG ACG GAT AAA GAC ATT CGC TAT ATT      4011
Asn Ile Asp Gln Leu Tyr Tyr Thr Thr Asp Lys Asp Ile Arg Tyr Ile
            800                 805                 810

ACT GAT AAA GTG AAT AAT ATG TAT CAA ACA ACC GTA GAA CTT GCC TAC      4059
Thr Asp Lys Val Asn Asn Met Tyr Gln Thr Thr Val Glu Leu Ala Tyr
        815                 820                 825

CGT TCT TTA CTT TTA CAA ACG CGT TTG AAG AAA TAT GTT TAT AGC GTT      4107
Arg Ser Leu Leu Leu Gln Thr Arg Leu Lys Lys Tyr Val Tyr Ser Val
    830                 835                 840

AAT GCG AAA CAA TTC GAA GGG AAA TGG GTA ACC GAT TAT TCT CGT ACT      4155
Asn Ala Lys Gln Phe Glu Gly Lys Trp Val Thr Asp Tyr Ser Arg Thr
845                 850                 855                 860

GAA GCC TTA TTT AAC TCT ACT TTT AAA CAA TCG CCT GAA AAT GCA TTA      4203
Glu Ala Leu Phe Asn Ser Thr Phe Lys Gln Ser Pro Glu Asn Ala Leu
                865                 870                 875

TAT GAT TTA AGC GAA TAC CTT TCT TTC TTT AAC GAT CCT ACG GAA TGG      4251
Tyr Asp Leu Ser Glu Tyr Leu Ser Phe Phe Asn Asp Pro Thr Glu Trp
            880                 885                 890

AAA GAA GGG CTA TTA CTG TTA AGC CGT TAT ATA GAT TAT GCT AAA GCA      4299
Lys Glu Gly Leu Leu Leu Leu Ser Arg Tyr Ile Asp Tyr Ala Lys Ala
        895                 900                 905

CAA GGA TTT TAT GAA AAC TGG GCG GCT ACT TCT AAC TTA ACT ATT GCC      4347
Gln Gly Phe Tyr Glu Asn Trp Ala Ala Thr Ser Asn Leu Thr Ile Ala
    910                 915                 920
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CGT TTA AGA GAG GCT GGA GTA ATT TTT GCA GAA TCG ACG GAT TTA AAA      4395
Arg Leu Arg Glu Ala Gly Val Ile Phe Ala Glu Ser Thr Asp Leu Lys
925                 930                 935                 940

GGC GAT GAA AAA AAT AAT ATT TTG TTA GGT AGC CAA AAA GAT AAT AAC      4443
Gly Asp Glu Lys Asn Asn Ile Leu Leu Gly Ser Gln Lys Asp Asn Asn
                945                 950                 955

TTA TCG GGT AGT GCA GGT GAT GAT CTA CTT ATC GGC GGA GAG GGT AAT      4491
Leu Ser Gly Ser Ala Gly Asp Asp Leu Leu Ile Gly Gly Glu Gly Asn
            960                 965                 970

GAT ACG TTA AAA GGC AGC TAC GGT GCA GAC ACC TAT ATC TTT AGC AAA      4539
Asp Thr Leu Lys Gly Ser Tyr Gly Ala Asp Thr Tyr Ile Phe Ser Lys
        975                 980                 985

GGA CAC GGA CAG GAT ATC GTT TAT GAA GAT ACC AAT AAT GAT AAC CGC      4587
Gly His Gly Gln Asp Ile Val Tyr Glu Asp Thr Asn Asn Asp Asn Arg
    990                 995                 1000

GCA AGA GAT ATC GAC ACC TTA AAA TTT ACC GAT GTG AAT TAT GCG GAA      4635
Ala Arg Asp Ile Asp Thr Leu Lys Phe Thr Asp Val Asn Tyr Ala Glu
1005                1010                1015                1020

GTG AAG TTT CGA CGA GTA GAT AAT GAC TTA ATG TTA TTC GGT TAT CAT      4683
Val Lys Phe Arg Arg Val Asp Asn Asp Leu Met Leu Phe Gly Tyr His
                1025                1030                1035

GAT ACG GAT TCG GTC ACG GTA AAA TCC TTC TAC AGC CAT GTA GAT TAT      4731
Asp Thr Asp Ser Val Thr Val Lys Ser Phe Tyr Ser His Val Asp Tyr
            1040                1045                1050

CAA TTT GAC AAA TTG GAG TTT GCT GAC CGC AGT ATA ACT CGC GAT GAA      4779
Gln Phe Asp Lys Leu Glu Phe Ala Asp Arg Ser Ile Thr Arg Asp Glu
        1055                1060                1065

CTG ATT AAA GCA GGG CTT CAT CTA TAC GGC ACC GAT GGC AAT GAT GAT      4827
Leu Ile Lys Ala Gly Leu His Leu Tyr Gly Thr Asp Gly Asn Asp Asp
    1070                1075                1080

ATA AAG GAT CAT GCG GAT TGG GAC AGC ATT TTG GAA GGC GGC AAA GGC      4875
Ile Lys Asp His Ala Asp Trp Asp Ser Ile Leu Glu Gly Gly Lys Gly
1085                1090                1095                1100

AAC GAT ATT CTA AGA GGT GGC TAC GGT GCG GAC ACC TAT ATC TTT AGC      4923
Asn Asp Ile Leu Arg Gly Gly Tyr Gly Ala Asp Thr Tyr Ile Phe Ser
                1105                1110                1115

AAA GGA CAC GGA CAG GAT ATC GTT TAT GAA GAT ACC AAT AAT GAT AAC      4971
Lys Gly His Gly Gln Asp Ile Val Tyr Glu Asp Thr Asn Asn Asp Asn
            1120                1125                1130

CGC GCA AGA GAT ATC GAC ACC TTA AAA TTT ACT GAT GTG AAT TAT GCG      5019
Arg Ala Arg Asp Ile Asp Thr Leu Lys Phe Thr Asp Val Asn Tyr Ala
        1135                1140                1145

GAA GTG AAA TTC CGA CGA GTA GAT AAT GAC TTA ATG TTA TTC GGT TAT      5067
Glu Val Lys Phe Arg Arg Val Asp Asn Asp Leu Met Leu Phe Gly Tyr
    1150                1155                1160

CAT GAT ACG GAT TCG GTC ACG ATA AAA TCC TTC TAC AAC CAT GTA GAT      5115
His Asp Thr Asp Ser Val Thr Ile Lys Ser Phe Tyr Asn His Val Asp
1165                1170                1175                1180

TAT CAA TTT GAC AAA TTG GAA TTT GCT GAC CGC AGT ATA ACT CGT GAT      5163
Tyr Gln Phe Asp Lys Leu Glu Phe Ala Asp Arg Ser Ile Thr Arg Asp
                1185                1190                1195
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GAA CTA GGT AAA CAA GGT ATG GCA TTA TTT GGC ACT GAC GGT GAT GAT      5211
Glu Leu Gly Lys Gln Gly Met Ala Leu Phe Gly Thr Asp Gly Asp Asp
            1200                1205                1210

AAT ATC AAC GAC TGG GGA CGT AAC TCG GTG ATT GAT GCC GGT GCG GGT      5259
Asn Ile Asn Asp Trp Gly Arg Asn Ser Val Ile Asp Ala Gly Ala Gly
        1215                1220                1225

AAT GAT ACG GTT AAT GGC GGT AAT GGC GAT GAC ACC CTC ATC GGC GGC      5307
Asn Asp Thr Val Asn Gly Gly Asn Gly Asp Asp Thr Leu Ile Gly Gly
    1230                1235                1240

AAA GGT AAT GAT ATT CTA AGA GGT GGC TAC GGT GCG GAC ACC TAT ATC      5355
Lys Gly Asn Asp Ile Leu Arg Gly Gly Tyr Gly Ala Asp Thr Tyr Ile
1245                1250                1255                1260

TTT AGC AAA GGA CAC GGA CAG GAT ATC GTT TAT GAA GAT ACC AAT AAT      5403
Phe Ser Lys Gly His Gly Gln Asp Ile Val Tyr Glu Asp Thr Asn Asn
                1265                1270                1275

GAT AAC CGC GCA AGA GAT ATC GAC ACC TTA AAA TTT ACC GAT GTG AAT      5451
Asp Asn Arg Ala Arg Asp Ile Asp Thr Leu Lys Phe Thr Asp Val Asn
            1280                1285                1290

TAT GCG GAA GTG AAA TTC CGA CGA GTA GAT AAT GAC TTA ATG TTA TTC      5499
Tyr Ala Glu Val Lys Phe Arg Arg Val Asp Asn Asp Leu Met Leu Phe
        1295                1300                1305

GGT TAT CAT GAT ACG GAT TCG GTC ACG GTA AAA TCC TTC TAC AGC CAT      5547
Gly Tyr His Asp Thr Asp Ser Val Thr Val Lys Ser Phe Tyr Ser His
    1310                1315                1320

GTA GAT TAT CAA TTT GAC AAA TTG GAG TTT GCT GAC CGC AGT ATA ACT      5595
Val Asp Tyr Gln Phe Asp Lys Leu Glu Phe Ala Asp Arg Ser Ile Thr
1325                1330                1335                1340

CGC GAT GAA CTG ATT AAA GCA GGG CTT CAT CTA TAC GGC ACC GAT GGC      5643
Arg Asp Glu Leu Ile Lys Ala Gly Leu His Leu Tyr Gly Thr Asp Gly
                1345                1350                1355

AAT GAT GAT ATA AAG GAT CAT GCG GAT TGG GAC AGC ATT TTG GAA GGC      5691
Asn Asp Asp Ile Lys Asp His Ala Asp Trp Asp Ser Ile Leu Glu Gly
            1360                1365                1370

GGC AAA GGC AAC GAT ATT CTA AGA GGT GGC TAC GGT GCG GAC ACC TAT      5739
Gly Lys Gly Asn Asp Ile Leu Arg Gly Gly Tyr Gly Ala Asp Thr Tyr
        1375                1380                1385

ATC TTT AGC AAA GGA CAC GGA CAG GAT ATC GTT TAT GAA GAT ACC AAT      5787
Ile Phe Ser Lys Gly His Gly Gln Asp Ile Val Tyr Glu Asp Thr Asn
    1390                1395                1400

AAT GAT AAC CGA GCA AGA GAT ATC GAC ACC TTA AAA TTT ACT GAT GTG      5835
Asn Asp Asn Arg Ala Arg Asp Ile Asp Thr Leu Lys Phe Thr Asp Val
1405                1410                1415                1420

AAT TAT GCG GAA GTG AAA TTC CGA CGA GTA GAT AAT GAC TTA ATG TTA      5883
Asn Tyr Ala Glu Val Lys Phe Arg Arg Val Asp Asn Asp Leu Met Leu
                1425                1430                1435

TTC GGT TAT CAT GAT ACG GAT TCG GTC ACG ATA AAA TCC TTC TAC AAC      5931
Phe Gly Tyr His Asp Thr Asp Ser Val Thr Ile Lys Ser Phe Tyr Asn
            1440                1445                1450

CAT GTA GAT TAT CAA TTT GAC AAA TTG GAA TTT GCT GAC CGC AGT ATA      5979
His Val Asp Tyr Gln Phe Asp Lys Leu Glu Phe Ala Asp Arg Ser Ile
        1455                1460                1465
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ACT CGT GAT GAA CTA GGT AAA CAA GGT ATG GCA TTA TTT GGC ACT GAC      6027
Thr Arg Asp Glu Leu Gly Lys Gln Gly Met Ala Leu Phe Gly Thr Asp
    1470                1475                1480

GGT GAT GAT AAT ATC AAC GAC TGG GGA CGT AAC TCG GTG ATT GAT GCC      6075
Gly Asp Asp Asn Ile Asn Asp Trp Gly Arg Asn Ser Val Ile Asp Ala
1485                1490                1495                1500

GGT GCG GGT AAT GAT ACG GTT AAT GGC GGT AAT GGC GAT GAC ACC CTC      6123
Gly Ala Gly Asn Asp Thr Val Asn Gly Gly Asn Gly Asp Asp Thr Leu
                1505                1510                1515

ATC GGC GGC AAA GGT AAT GAT ATT CTA AGA GGT GGC TAC GGT GCG GAC      6171
Ile Gly Gly Lys Gly Asn Asp Ile Leu Arg Gly Gly Tyr Gly Ala Asp
            1520                1525                1530

ACC TAT ATC TTT AGC AAA GGA CAC GGA CAG GAT ATC GTT TAT GAA GAT      6219
Thr Tyr Ile Phe Ser Lys Gly His Gly Gln Asp Ile Val Tyr Glu Asp
        1535                1540                1545

ACC AAT AAT GAT AAC CGC GCA AGA GAT ATC GAC ACC TTA AAA TTT ACT      6267
Thr Asn Asn Asp Asn Arg Ala Arg Asp Ile Asp Thr Leu Lys Phe Thr
    1550                1555                1560

GAT ATT AAT TTA TCC GAA CTT TGG TTT AGC CGA GAA AAT AAC GAT TTG      6315
Asp Ile Asn Leu Ser Glu Leu Trp Phe Ser Arg Glu Asn Asn Asp Leu
1565                1570                1575                1580

ATT ATT AAA TCA TTA TTA AGT GAG GAT AAA GTC ACG GTT CAA AAT TGG      6363
Ile Ile Lys Ser Leu Leu Ser Glu Asp Lys Val Thr Val Gln Asn Trp
                1585                1590                1595

TAT TCA CAC CAA GAT CAT AAA ATA GAA AAT ATT CGT TTA TCG AAT GAG      6411
Tyr Ser His Gln Asp His Lys Ile Glu Asn Ile Arg Leu Ser Asn Glu
            1600                1605                1610

CAA ACG TTG GTG AGC ACT CAG GTG GAG AAG ATG GTT GAG TCG ATG GCC      6459
Gln Thr Leu Val Ser Thr Gln Val Glu Lys Met Val Glu Ser Met Ala
        1615                1620                1625

GGC TTT GCT CAG AAG CAC GGA GGA GAG ATA TCT CTT GTG TCG CTT GAA      6507
Gly Phe Ala Gln Lys His Gly Gly Glu Ile Ser Leu Val Ser Leu Glu
    1630                1635                1640

GAG GTA AAA CAA TAT ATC AAT AGC TTA ACA GCT GCT TTA TAA              6549
Glu Val Lys Gln Tyr Ile Asn Ser Leu Thr Ala Ala Leu  *
1645                1650                1655

CATACGAAAG AAATCGGCAC AGTTTTTTTG AACTGTGCCG ATTTGATTTT AGTGTAAGAA    6609

TATAGCCTGA TTTTAAGAAA TTTACTCTTG GCTAATAACT ATTTCCCATT TTATAAGTTA    6669

TTGACGGATG GTTTTATCAA ATATGAGATC AAATCTTATT TTAAATTCGC TTTCCATTAA    6729

GCGATAT                                                             6736
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(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1658 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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Met Ser Asp Asn Ala Phe Phe Val Ile Glu Glu Ser Gly Lys Arg Tyr
 1               5                  10                  15

Ile Glu Asn Phe Gly Ile Glu Pro Leu Gly Lys Gln Glu Asp Phe Asp
            20                  25                  30

Phe Val Gly Gly Phe Trp Ser Asn Leu Val Asn Arg Gly Leu Glu Ser
        35                  40                  45

Ile Ile Asp Pro Ser Gly Ile Gly Gly Thr Val Asn Leu Asn Phe Thr
    50                  55                  60

Gly Glu Val Glu Thr Tyr Thr Leu Asp Glu Thr Arg Phe Lys Ala Glu
65                  70                  75                  80

Ala Ala Lys Lys Ser His Trp Ser Leu Val Asn Ala Ala Lys Val Tyr
                85                  90                  95

Gly Gly Leu Asp Gln Ile Ile Lys Lys Leu Trp Asp Ser Gly Ser Ile
            100                 105                 110

Lys His Leu Tyr Gln Asp Lys Asp Thr Gly Lys Leu Lys Pro Ile Ile
        115                 120                 125

Tyr Gly Thr Ala Gly Asn Asp Ser Lys Ile Glu Gly Thr Lys Ile Thr
    130                 135                 140

Arg Arg Ile Ala Gly Lys Glu Val Thr Leu Asp Ile Ala Asn Gln Lys
145                 150                 155                 160

Ile Glu Lys Gly Val Leu Glu Lys Leu Gly Leu Ser Val Ser Gly Ser
                165                 170                 175

Asp Ile Ile Lys Leu Leu Phe Gly Ala Leu Thr Pro Thr Leu Asn Arg
            180                 185                 190

Met Leu Leu Ser Gln Leu Ile Gln Ser Phe Ser Asp Ser Leu Ala Lys
        195                 200                 205

Leu Asp Asn Pro Leu Ala Pro Tyr Thr Lys Asn Gly Val Val Tyr Val
    210                 215                 220

Thr Gly Lys Gly Asn Asp Val Leu Lys Gly Thr Glu His Glu Asp Leu
225                 230                 235                 240

Phe Leu Gly Gly Glu Gly Asn Asp Thr Tyr Tyr Ala Arg Val Gly Asp
                245                 250                 255

Thr Ile Glu Asp Ala Asp Gly Lys Gly Lys Val Tyr Phe Val Arg Glu
            260                 265                 270

Lys Gly Val Pro Lys Ala Asp Pro Lys Arg Val Glu Phe Ser Glu Tyr
        275                 280                 285

Ile Thr Lys Glu Glu Ile Lys Glu Val Glu Lys Gly Leu Leu Thr Tyr
    290                 295                 300

Ala Val Leu Glu Asn Tyr Asn Trp Glu Glu Lys Thr Ala Thr Phe Ala
305                 310                 315                 320
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His Ala Thr Met Leu Asn Glu Leu Phe Thr Asp Tyr Thr Asn Tyr Arg
325 330 335

Tyr Glu Val Lys Gly Leu Lys Leu Pro Ala Val Lys Lys Leu Lys Ser
340 345 350

Pro Leu Val Glu Phe Thr Ala Asp Leu Leu Thr Val Thr Pro Ile Asp
355 360 365

Glu Asn Gly Lys Ala Leu Ser Glu Lys Ser Ile Thr Val Lys Asn Phe
370 375 380

Lys Asn Gly Asp Leu Gly Ile Arg Leu Leu Asp Pro Asn Ser Tyr Tyr
385 390 395 400

Tyr Phe Leu Glu Gly Gln Asp Thr Gly Phe Tyr Gly Pro Ala Phe Tyr
405 410 415

Ile Glu Arg Lys Asn Gly Gly Gly Ala Lys Asn Asn Ser Ser Gly Ala
420 425 430

Gly Asn Ser Lys Asp Trp Gly Gly Asn Gly His Gly Asn His Arg Asn
435 440 445

Asn Ala Ser Asp Leu Asn Lys Pro Asp Gly Asn Asn Gly Asn Asn Gln
450 455 460

Asn Asn Gly Ser Asn Gln Asp Asn His Ser Asp Val Asn Ala Pro Asn
465 470 475 480

Asn Pro Gly Arg Asn Tyr Asp Ile Tyr Asp Pro Leu Ala Leu Asp Leu
485 490 495

Asp Gly Asp Gly Leu Glu Thr Val Ser Met Asn Gly Arg Gln Gly Ala
500 505 510

Leu Phe Asp His Glu Gly Lys Gly Ile Arg Thr Ala Thr Gly Trp Leu
515 520 525

Ala Ala Asp Asp Gly Phe Leu Val Leu Asp Arg Asn Gln Asp Gly Ile
530 535 540

Ile Asn Asp Ile Ser Glu Leu Phe Ser Asn Lys Asn Gln Leu Ser Asp
545 550 555 560

Gly Ser Ile Ser Ala His Gly Phe Ala Thr Leu Ala Asp Leu Asp Thr
565 570 575

Asn Gln Asp Gln Arg Ile Asp Gln Asn Asp Lys Leu Phe Ser Lys Leu
580 585 590

Gln Ile Trp Arg Asp Leu Asn Gln Asn Gly Phe Ser Glu Ala Asn Glu
595 600 605

Leu Phe Ser Leu Glu Ser Leu Asn Ile Lys Ser Leu His Thr Ala Tyr
610 615 620

Glu Glu Arg Asn Asp Phe Leu Ala Gly Asn Asn Ile Leu Ala Gln Leu
625 630 635 640

Gly Lys Tyr Glu Lys Thr Asp Gly Thr Phe Ala Gln Met Gly Asp Leu
645 650 655

Asn Phe Ser Phe Asn Pro Phe Tyr Ser Arg Phe Thr Glu Ala Leu Asn
660 665 670

Leu Thr Glu Gln Gln Arg Arg Thr Ile Asn Leu Thr Gly Thr Gly Arg
675 680 685

Val Arg Asp Leu Arg Glu Ala Ala Ala Leu Ser Glu Glu Leu Ala Ala
690 695 700

Leu Leu Gln Gln Tyr Thr Lys Ala Ser Asp Phe Gln Ala Gln Arg Glu
705 710 715 720

Leu Leu Pro Ala Ile Leu Asp Lys Trp Ala Ala Thr Asp Leu Gln Tyr
725 730 735

Gln His Tyr Asp Lys Thr Leu Leu Lys Thr Val Glu Ser Thr Asp Ser
740 745 750

Ser Ala Ser Val Val Arg Val Thr Pro Ser Gln Leu Ser Ser Ile Arg
755 760 765

Asn Ala Lys His Asp Pro Thr Val Met Gln Asn Phe Glu Gln Ser Lys
770 775 780

Ala Lys Ile Ala Thr Leu Asn Ser Leu Tyr Gly Leu Asn Ile Asp Gln
785 790 795 800

Leu Tyr Tyr Thr Thr Asp Lys Asp Ile Arg Tyr Ile Thr Asp Lys Val
805 810 815

Asn Asn Met Tyr Gln Thr Thr Val Glu Leu Ala Tyr Arg Ser Leu Leu
820 825 830

Leu Gln Thr Arg Leu Lys Lys Tyr Val Tyr Ser Val Asn Ala Lys Gln
835 840 845

Phe Glu Gly Lys Trp Val Thr Asp Tyr Ser Arg Thr Glu Ala Leu Phe
850 855 860

Asn Ser Thr Phe Lys Gln Ser Pro Glu Asn Ala Leu Tyr Asp Leu Ser
865 870 875 880

Glu Tyr Leu Ser Phe Phe Asn Asp Pro Thr Glu Trp Lys Glu Gly Leu
885 890 895

Leu Leu Leu Ser Arg Tyr Ile Asp Tyr Ala Lys Ala Gln Gly Phe Tyr
900 905 910

Glu Asn Trp Ala Ala Thr Ser Asn Leu Thr Ile Ala Arg Leu Arg Glu
915 920 925

Ala Gly Val Ile Phe Ala Glu Ser Thr Asp Leu Lys Gly Asp Glu Lys
930 935 940

Asn Asn Ile Leu Leu Gly Ser Gln Lys Asp Asn Asn Leu Ser Gly Ser
945 950 955 960

Ala Gly Asp Asp Leu Leu Ile Gly Gly Glu Gly Asn Asp Thr Leu Lys
965 970 975

Gly Ser Tyr Gly Ala Asp Thr Tyr Ile Phe Ser Lys Gly His Gly Gln
980 985 990

Asp Ile Val Tyr Glu Asp Thr Asn Asn Asp Asn Arg Ala Arg Asp Ile
995 1000 1005

Asp Thr Leu Lys Phe Thr Asp Val Asn Tyr Ala Glu Val Lys Phe Arg
1010 1015 1020

Arg Val Asp Asn Asp Leu Met Leu Phe Gly Tyr His Asp Thr Asp Ser
1025 1030 1035 1040

Val Thr Val Lys Ser Phe Tyr Ser His Val Asp Tyr Gln Phe Asp Lys
1045 1050 1055

Leu Glu Phe Ala Asp Arg Ser Ile Thr Arg Asp Glu Leu Ile Lys Ala
1060 1065 1070

Gly Leu His Leu Tyr Gly Thr Asp Gly Asn Asp Asp Ile Lys Asp His
1075 1080 1085

Ala Asp Trp Asp Ser Ile Leu Glu Gly Gly Lys Gly Asn Asp Ile Leu
1090 1095 1100

Arg Gly Gly Tyr Gly Ala Asp Thr Tyr Ile Phe Ser Lys Gly His Gly
1105 1110 1115 1120

Gln Asp Ile Val Tyr Glu Asp Thr Asn Asn Asp Asn Arg Ala Arg Asp
1125 1130 1135

Ile Asp Thr Leu Lys Phe Thr Asp Val Asn Tyr Ala Glu Val Lys Phe
1140 1145 1150

Arg Arg Val Asp Asn Asp Leu Met Leu Phe Gly Tyr His Asp Thr Asp
1155 1160 1165

Ser Val Thr Ile Lys Ser Phe Tyr Asn His Val Asp Tyr Gln Phe Asp
1170 1175 1180

Lys Leu Glu Phe Ala Asp Arg Ser Ile Thr Arg Asp Glu Leu Gly Lys
1185 1190 1195 1200

Gln Gly Met Ala Leu Phe Gly Thr Asp Gly Asp Asp Asn Ile Asn Asp
1205 1210 1215

Trp Gly Arg Asn Ser Val Ile Asp Ala Gly Ala Gly Asn Asp Thr Val
1220 1225 1230

Asn Gly Gly Asn Gly Asp Asp Thr Leu Ile Gly Gly Lys Gly Asn Asp
1235 1240 1245

Ile Leu Arg Gly Gly Tyr Gly Ala Asp Thr Tyr Ile Phe Ser Lys Gly
1250 1255 1260

His Gly Gln Asp Ile Val Tyr Glu Asp Thr Asn Asn Asp Asn Arg Ala
1265 1270 1275 1280

Arg Asp Ile Asp Thr Leu Lys Phe Thr Asp Val Asn Tyr Ala Glu Val
1285 1290 1295

Lys Phe Arg Arg Val Asp Asn Asp Leu Met Leu Phe Gly Tyr His Asp
1300 1305 1310

Thr Asp Ser Val Thr Val Lys Ser Phe Tyr Ser His Val Asp Tyr Gln
1315 1320 1325

Phe Asp Lys Leu Glu Phe Ala Asp Arg Ser Ile Thr Arg Asp Glu Leu
1330 1335 1340

Ile Lys Ala Gly Leu His Leu Tyr Gly Thr Asp Gly Asn Asp Asp Ile
1345 1350 1355 1360

Lys Asp His Ala Asp Trp Asp Ser Ile Leu Glu Gly Gly Lys Gly Asn
1365 1370 1375

Asp Ile Leu Arg Gly Gly Tyr Gly Ala Asp Thr Tyr Ile Phe Ser Lys
1380 1385 1390

Gly His Gly Gln Asp Ile Val Tyr Glu Asp Thr Asn Asn Asp Asn Arg
1395 1400 1405

Ala Arg Asp Ile Asp Thr Leu Lys Phe Thr Asp Val Asn Tyr Ala Glu
1410 1415 1420

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Val Lys Phe Arg Arg Val Asp Asn Asp Leu Met Leu Phe Gly Tyr His
1425                1430                1435                1440

Asp Thr Asp Ser Val Thr Ile Lys Ser Phe Tyr Asn His Val Asp Tyr
                1445                1450                1455

Gln Phe Asp Lys Leu Glu Phe Ala Asp Arg Ser Ile Thr Arg Asp Glu
            1460                1465                1470

Leu Gly Lys Gln Gly Met Ala Leu Phe Gly Thr Asp Gly Asp Asp Asn
        1475                1480                1485

Ile Asn Asp Trp Gly Arg Asn Ser Val Ile Asp Ala Gly Ala Gly Asn
    1490                1495                1500

Asp Thr Val Asn Gly Gly Asn Gly Asp Asp Thr Leu Ile Gly Gly Lys
1505                1510                1515                1520

Gly Asn Asp Ile Leu Arg Gly Gly Tyr Gly Ala Asp Thr Tyr Ile Phe
                1525                1530                1535

Ser Lys Gly His Gly Gln Asp Ile Val Tyr Glu Asp Thr Asn Asn Asp
            1540                1545                1550

Asn Arg Ala Arg Asp Ile Asp Thr Leu Lys Phe Thr Asp Ile Asn Leu
        1555                1560                1565

Ser Glu Leu Trp Phe Ser Arg Glu Asn Asn Asp Leu Ile Ile Lys Ser
    1570                1575                1580

Leu Leu Ser Glu Asp Lys Val Thr Val Gln Asn Trp Tyr Ser His Gln
1585                1590                1595                1600

Asp His Lys Ile Glu Asn Ile Arg Leu Ser Asn Glu Gln Thr Leu Val
                1605                1610                1615

Ser Thr Gln Val Glu Lys Met Val Glu Ser Met Ala Gly Phe Ala Gln
            1620                1625                1630

Lys His Gly Gly Glu Ile Ser Leu Val Ser Leu Glu Glu Val Lys Gln
        1635                1640                1645

Tyr Ile Asn Ser Leu Thr Ala Ala Leu  *
    1650                1655
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(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7004 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Actinobacillus pleuropneumoniae
(B) STRAIN: HV114 (serotype 3 field strain)

(vii) IMMEDIATE SOURCE:
(B) CLONE: pROK5

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1566..5714
(D) OTHER INFORMATION:/codon_start= 1566
/function= "RTX-toxin"
/product= "ApxIV_var3"
/gene= "apxIV_var3"
/number= 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATCGATATGC CGCCGGGTAC GGGCGATATC CAACTTACTC TTTCGCAACA AATTCCGGTT 60

ACCGGTGCGG TAGTGGTAAC TACTCCGCAA GATATTGCGT TATTAGATGC GGTGAAAGGT 120

ATTTCAATGT TCCAAAAAGT GTCGGTACCG GTCTTAGGTA TCATTGAAAA TATGAGCGTG 180

CATATCTGCC AAAATTGCGG TCACCACGAA GATATTTTCG GCACCGGCGG TGCGGAGAAA 240

GTGGCGAAGA AATACGGTAC TAAAGTATTA GGACAAATGC CGTTGCATAT TCGCTTACGT 300

CAAGATTTGG ATGCCGGCAC ACCGACCGTC GTTGCGGCAC CGGAACACGA CACCAGCAGA 360

GCCTATATTG AATTAGCGGC AAAAGTCGCT TCGGAATTAT ACTGGCAAGG TTCGGTTATC 420

CCGTCTGAAA TTATGATTCG TGAAGTAAAA TAAGCCTACA TAACCACGGA ATACCAGATA 480

ACACAGAAGG AAAACAAGCG GTAGAATTTG CAGAAAAAGT TGCAAATTCT ACCGCTTTTT 540

TATTAGTACG ATTCGCTGTT GGACTGCCAT TTGATTTGGT TTGTCAGGAT ATTATGTTAT 600

TGTAATGAAA TGTTAGTGAA TTATTTTTAT TAATTTGAAA GGAGACAAAA TGAAAATAAA 660

AAAACGTTAC ATTGCGCTGC TAGCTTTAGG CAGTGTTATT GGCTATGCCT GGTATCAAAA 720

TTATCAATGG GAACAGTTGA TGTTAAGTGG CTATTGTGAA AAGGACGGAA GCTATTGTGA 780

TGATAGGCAT ACGAAGCAGG AACTGATTGA TAGGGCAATT AACTATGTGC TGGAAAATCA 840

AATTCAACAG ACATATGAAG GTGATGACCT TGTGGATATA AAACAATATT CAACAATAGA 900

GGAATTTAAA AAACTAAATC CGAATTGTTG TAAGGTAGAT TCTTGGCCGG ATGATGCTGT 960

TCGTGAGGAT GCTGATTTAC AGCGAGAGGG CAAAGCGTAT AAATACGTAA AAGTCAAATA 1020

TTTAAGAACC TATTTAGCGA ATAGAGAACC TGAACAATGG GAAAATTACA TAGTATTTGA 1080

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TAATTGCAGT GGAATTAAAG AAAGACACCA ACTGTATTAA AAATAGATTA GATGGAGACA    1140

ACACGATGAC AAAACTAACT ATCCAAGATG TGACTAATTT ATATTTATAT AAGCAAAGAA    1200

CTTTACCTAC GGATAGGTTA GATGATTCGC TTATTAGCAA AACAGGAAAA GGGGAAAATA    1260

TTGATAAAAA GGAATTTATG GCGGGGCCGG GACGTTTTGT GACGGCCGAT AATTTTAGTG    1320

TTGTAAAAGA CTTTTTTACT GCAAAGGATT CATTAATAAA CCTAAGCTTG CAGACTCGTA    1380

TATTAGCGAA TTTAAAGCCG GGCAAATATT CCAAAGCGCA GATATTAGAA ATGTTGGGCT    1440

ATACGAAAAA TGGAGAAAAG GTAGATGGCA TGTTTACCGG TGAAGTCCAG ACATTAGGCT    1500

TTTATGACGA TGGCAAAGGG GATTTACTCG AACGCGCCTA TATCTGAAAT ACCACAGGAT    1560

TTAAA ATG AGC GAC AAT GCC TTT TTT GTT ATA GAA GAA TCA GGC AAA          1607
      Met Ser Asp Asn Ala Phe Phe Val Ile Glu Glu Ser Gly Lys
          1660                1665                1670

CGC TAT ATT GAA AAC TTT GGT ATT GAA CCT CTT GGT AAG CAA GAA GAT       1655
Arg Tyr Ile Glu Asn Phe Gly Ile Glu Pro Leu Gly Lys Gln Glu Asp
        1675                1680                1685

TTT GAT TTT GTC GGC GGC TTT TGG TCT AAC TTA GTG AAT CGT GGT TTG       1703
Phe Asp Phe Val Gly Gly Phe Trp Ser Asn Leu Val Asn Arg Gly Leu
    1690                1695                1700

GAA AGT ATT ATC GAC CCA TCC GGT ATC GGT GGA ACG GTA AAC CTT AAC       1751
Glu Ser Ile Ile Asp Pro Ser Gly Ile Gly Gly Thr Val Asn Leu Asn
1705                1710                1715                1720

TTT ACC GGC GAG GTG GAA ACC TAC ACG TTA GAC GAA ACA AGG TTT AAA       1799
Phe Thr Gly Glu Val Glu Thr Tyr Thr Leu Asp Glu Thr Arg Phe Lys
                1725                1730                1735

GCG GAA GCG GCG AAG AAA AGC CAT TGG AGT TTA GTG AAT GCG GCG AAA       1847
Ala Glu Ala Ala Lys Lys Ser His Trp Ser Leu Val Asn Ala Ala Lys
            1740                1745                1750

GTA TAC GGC GGT TTA GAC CAA ATT ATT AAA AAA CTA TGG GAC AGT GGC       1895
Val Tyr Gly Gly Leu Asp Gln Ile Ile Lys Lys Leu Trp Asp Ser Gly
        1755                1760                1765

TCA ATT AAG CAT TTA TAT CAA GAT AAA GAT ACG GGC AAA TTA AAA CCG       1943
Ser Ile Lys His Leu Tyr Gln Asp Lys Asp Thr Gly Lys Leu Lys Pro
    1770                1775                1780

ATT ATT TAC GGC ACG GCC GGC AAC GAC AGT AAG ATT GAA GGC ACT AAA       1991
Ile Ile Tyr Gly Thr Ala Gly Asn Asp Ser Lys Ile Glu Gly Thr Lys
1785                1790                1795                1800

ATC ACC CGT AGG ATT GCG GGT AAA GAA GTT ACG CTT GAT ATT GCC AAT       2039
Ile Thr Arg Arg Ile Ala Gly Lys Glu Val Thr Leu Asp Ile Ala Asn
                1805                1810                1815

CAG AAA ATT GAA AAA GGC GTG TTA GAG AAA TTG GGG CTG TCT GTT AGT       2087
Gln Lys Ile Glu Lys Gly Val Leu Glu Lys Leu Gly Leu Ser Val Ser
            1820                1825                1830

GGT TCG GAT ATC ATT AAA TTG TTG TTT GGA GCA TTG ACT CCA ACT TTA       2135
Gly Ser Asp Ile Ile Lys Leu Leu Phe Gly Ala Leu Thr Pro Thr Leu
        1835                1840                1845

AAT AGA ATG TTG CTA TCA CAA CTT ATC CAG TCT TTT TCC GAT AGC TTG       2183
Asn Arg Met Leu Leu Ser Gln Leu Ile Gln Ser Phe Ser Asp Ser Leu
    1850                1855                1860
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GCT AAA CTT GAT AAT CCC TTA GCC CCT TAC ACT AAA AAT GGC GTG GTT      2231
Ala Lys Leu Asp Asn Pro Leu Ala Pro Tyr Thr Lys Asn Gly Val Val
1865                1870                1875                1880

TAT GTC ACC GGC AAA GGG AAT GAT GTG CTT AAA GGA ACT GAA CAT GAG      2279
Tyr Val Thr Gly Lys Gly Asn Asp Val Leu Lys Gly Thr Glu His Glu
                1885                1890                1895

GAT TTG TTT CTC GGT GGT GAG GGG AAT GAT ACT TAT TAT GCG AGA GTA      2327
Asp Leu Phe Leu Gly Gly Glu Gly Asn Asp Thr Tyr Tyr Ala Arg Val
        1900                1905                1910

GGC GAT ACA ATT GAA GAC GCC GAC GGC AAA GGT AAA GTC TAT TTT GTG      2375
Gly Asp Thr Ile Glu Asp Ala Asp Gly Lys Gly Lys Val Tyr Phe Val
        1915                1920                1925

AGA GAA AAA GGG GTA CCT AAG GCG GAT CCT AAG CGG GTA GAG TTT AGC      2423
Arg Glu Lys Gly Val Pro Lys Ala Asp Pro Lys Arg Val Glu Phe Ser
    1930                1935                1940

GAG TAC ATA ACG AAA GAA GAA ATA AAA GAG GTT GAA AAG GGG TTA TTA      2471
Glu Tyr Ile Thr Lys Glu Glu Ile Lys Glu Val Glu Lys Gly Leu Leu
1945                1950                1955                1960

ACT TAC GCA GTT TTA GAA AAT TAT AAT TGG GAA GAG AAA ACG GCG ACT      2519
Thr Tyr Ala Val Leu Glu Asn Tyr Asn Trp Glu Glu Lys Thr Ala Thr
                1965                1970                1975

TTC GCT CAT GCG ACT ATG CTT AAT GAG CTT TTT ACT GAT TAT ACT AAT      2567
Phe Ala His Ala Thr Met Leu Asn Glu Leu Phe Thr Asp Tyr Thr Asn
        1980                1985                1990

TAT CGT TAT GAA GTT AAA GGA CTA AAA TTG CCC GCC GTT AAA AAG TTA      2615
Tyr Arg Tyr Glu Val Lys Gly Leu Lys Leu Pro Ala Val Lys Lys Leu
        1995                2000                2005

AAA AGT CCG TTG GTG GAG TTT ACA GCT GAT TTA TTA ACT GTT ACG CCT      2663
Lys Ser Pro Leu Val Glu Phe Thr Ala Asp Leu Leu Thr Val Thr Pro
    2010                2015                2020

ATT GAC GAA AAC GGA AAA GCA CTT AGC GAA AAA AGT ATT ACG GTT AAA      2711
Ile Asp Glu Asn Gly Lys Ala Leu Ser Glu Lys Ser Ile Thr Val Lys
2025                2030                2035                2040

AAT TTT AAA AAT GGT GAT TTA GGA ATA AGG TTG TTG GAT CCT AAT AGC      2759
Asn Phe Lys Asn Gly Asp Leu Gly Ile Arg Leu Leu Asp Pro Asn Ser
                2045                2050                2055

TAT TAT TAT TTC CTT GAA GGC CAA GAT ACG GGT TTT TAT GGT CCT GCT      2807
Tyr Tyr Tyr Phe Leu Glu Gly Gln Asp Thr Gly Phe Tyr Gly Pro Ala
        2060                2065                2070

TTT TAT ATT GAA CGA AAA AAC GGT GGA GGC TCT AAA AAT AAC TCG TCG      2855
Phe Tyr Ile Glu Arg Lys Asn Gly Gly Gly Ser Lys Asn Asn Ser Ser
        2075                2080                2085

GGA GCA GGA AAT AGC AAA GAT TGG GGC GGG AAC GGG CAT GGA AAT CAC      2903
Gly Ala Gly Asn Ser Lys Asp Trp Gly Gly Asn Gly His Gly Asn His
    2090                2095                2100

CGA AAT AAT GCC TCC GAC CTG AAT AAA CCG GAC GGA AAT AAT GGG AAT      2951
Arg Asn Asn Ala Ser Asp Leu Asn Lys Pro Asp Gly Asn Asn Gly Asn
2105                2110                2115                2120

AAC CAA AAT AAC GGA AGC AAT CAA GAT AAT CAT AGC GAT GTG AAT GCG      2999
Asn Gln Asn Asn Gly Ser Asn Gln Asp Asn His Ser Asp Val Asn Ala
                2125                2130                2135
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CCA AAT AAC CCG GGA CGT AAC TAT GAT ATT TAC GAT CCT TTA GCT TTA      3047
Pro Asn Asn Pro Gly Arg Asn Tyr Asp Ile Tyr Asp Pro Leu Ala Leu
            2140                2145                2150

GAT TTA GAT GGA GAT GGG CTT GAA ACC GTG TCG ATG AAC GGG CGA CAA      3095
Asp Leu Asp Gly Asp Gly Leu Glu Thr Val Ser Met Asn Gly Arg Gln
        2155                2160                2165

GGC GCG TTA TTC GAT CAT GAA GGA AAA GGT ATT CGT ACC GCA ACG GGC      3143
Gly Ala Leu Phe Asp His Glu Gly Lys Gly Ile Arg Thr Ala Thr Gly
    2170                2175                2180

TGG CTC GCT GCG GAT GAC GGT TTT TTA GTG TTA GAT CGT AAC CAA GAC      3191
Trp Leu Ala Ala Asp Asp Gly Phe Leu Val Leu Asp Arg Asn Gln Asp
2185                2190                2195                2200

GGC ATT ATT AAT GAT ATA AGC GAG TTA TTT AGT AAT AAA AAT CAA CTT      3239
Gly Ile Ile Asn Asp Ile Ser Glu Leu Phe Ser Asn Lys Asn Gln Leu
                2205                2210                2215

TCC GAC GGG AGT ATT TCT GCA CAC GGT TTT GCG ACA TTA GCC GAT TTG      3287
Ser Asp Gly Ser Ile Ser Ala His Gly Phe Ala Thr Leu Ala Asp Leu
            2220                2225                2230

GAT ACA AAC CAA GAT CAG CGT ATC GAC CAA AAT GAT AAG CTG TTT TCT      3335
Asp Thr Asn Gln Asp Gln Arg Ile Asp Gln Asn Asp Lys Leu Phe Ser
        2235                2240                2245

AAA CTC CAA ATT TGG CGG GAT TTA AAT CAA AAC GGT TTT AGT GAA GCG      3383
Lys Leu Gln Ile Trp Arg Asp Leu Asn Gln Asn Gly Phe Ser Glu Ala
    2250                2255                2260

AAT GAG CTG TTT AGC TTA GAA AGT TTG AAT ATT AAA TCT TTA CAT ACC      3431
Asn Glu Leu Phe Ser Leu Glu Ser Leu Asn Ile Lys Ser Leu His Thr
2265                2270                2275                2280

GCC TAT GAA GAG CGT AAT GAT TTT CTA GCG GGC AAT AAT ATC CTT GCT      3479
Ala Tyr Glu Glu Arg Asn Asp Phe Leu Ala Gly Asn Asn Ile Leu Ala
                2285                2290                2295

CAG CTT GGG AAG TAT GAA AAA ACG GAC GGT ACT TTT GGA CAA ATG GGC      3527
Gln Leu Gly Lys Tyr Glu Lys Thr Asp Gly Thr Phe Gly Gln Met Gly
            2300                2305                2310

GAT TTA AAT TTC AGT TTT AAC CCG TTT TAT AGC CGA TTT ACC GAA GCG      3575
Asp Leu Asn Phe Ser Phe Asn Pro Phe Tyr Ser Arg Phe Thr Glu Ala
        2315                2320                2325

TTA AAT TTA ACC GAG CAA CAA CGT CGC ACA ATT AAT CTA ACC GGC ACC      3623
Leu Asn Leu Thr Glu Gln Gln Arg Arg Thr Ile Asn Leu Thr Gly Thr
    2330                2335                2340

GGT CGG GTT CGG GAT TTG CGT GAA GCC GCC GCA CTT TCT GAG GAG TTG      3671
Gly Arg Val Arg Asp Leu Arg Glu Ala Ala Ala Leu Ser Glu Glu Leu
2345                2350                2355                2360

GCT GCT TTA TTA CAA CAG TAC ACT AAG GGC TCC GAT TTT CAG GCA CAA      3719
Ala Ala Leu Leu Gln Gln Tyr Thr Lys Gly Ser Asp Phe Gln Ala Gln
                2365                2370                2375

CGA GAA TTA TTG CCT GCC ATT TTA GAT AAA TGG GCG GCA ACG GAT TTA      3767
Arg Glu Leu Leu Pro Ala Ile Leu Asp Lys Trp Ala Ala Thr Asp Leu
            2380                2385                2390

CAG TAT CAA CAT TAT GAT AAA ACA TTA CTT AAA ACG GTA GAA AGT ACC      3815
Gln Tyr Gln His Tyr Asp Lys Thr Leu Leu Lys Thr Val Glu Ser Thr
        2395                2400                2405
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GAT AGT AGT GCT TCT GTC GTT AGA GTC ACG CCT TCT CAA TTA AGT AGT      3863
Asp Ser Ser Ala Ser Val Val Arg Val Thr Pro Ser Gln Leu Ser Ser
    2410                2415                2420

ATA CGC AAT GTA AAG CAT GAT CCT ACC GTT ATG CAA AAC TGT GAA CAA      3911
Ile Arg Asn Val Lys His Asp Pro Thr Val Met Gln Asn Cys Glu Gln
2425                2430                2435                2440

AGT AAG GCA AAA ATT GCG ACT TTA AAT TCG CTC TAC GGG TTA AAT ATT      3959
Ser Lys Ala Lys Ile Ala Thr Leu Asn Ser Leu Tyr Gly Leu Asn Ile
                2445                2450                2455

GAT CAA CTT TAT TAT ACG ACG GAT AAA GAC ATT CGT TAT ATT ACT GAC      4007
Asp Gln Leu Tyr Tyr Thr Thr Asp Lys Asp Ile Arg Tyr Ile Thr Asp
            2460                2465                2470

AAA GTG AAT AAT ATG TAT CAA ACA ACC GGA GAA CTC GGC TAT CGT TCT      4055
Lys Val Asn Asn Met Tyr Gln Thr Thr Gly Glu Leu Gly Tyr Arg Ser
        2475                2480                2485

TTA CTT TTA CAA ACG CGT GTG AAG AAA TAT GTT TAT AGC GTT AAT GCG      4103
Leu Leu Leu Gln Thr Arg Val Lys Lys Tyr Val Tyr Ser Val Asn Ala
    2490                2495                2500

AAA CAA TTC GAA GGG AAA TGG GTA GCC GAT TAT TCT CGT ACT GAA GCC      4151
Lys Gln Phe Glu Gly Lys Trp Val Ala Asp Tyr Ser Arg Thr Glu Ala
2505                2510                2515                2520

TTA TTT AAC TCT ACT TAT AAA CAA TCG CCC GAA AAT GTA TTA TAT GAT      4199
Leu Phe Asn Ser Thr Tyr Lys Gln Ser Pro Glu Asn Val Leu Tyr Asp
                2525                2530                2535

TTA CGC GAA TAC CTT TCT TTC TAT AAC GAC CCT ACG GAA TGG AAA GAA      4247
Leu Arg Glu Tyr Leu Ser Phe Tyr Asn Asp Pro Thr Glu Trp Lys Glu
            2540                2545                2550

GGG CTA TTA CTG TTA AGC CGT TAT ATA GAT TAT GCT AAA GCA CAA GGA      4295
Gly Leu Leu Leu Leu Ser Arg Tyr Ile Asp Tyr Ala Lys Ala Gln Gly
        2555                2560                2565

TTT TAT GAA AAC TGG GCG GCT ACT TCT AAC TTA ACT ATT GCC CGT TTA      4343
Phe Tyr Glu Asn Trp Ala Ala Thr Ser Asn Leu Thr Ile Ala Arg Leu
    2570                2575                2580

AGA GAG GCT GGA GTA ATT TGT GCA GAA TCG ACG GAT TTA AAA GGC GAT      4391
Arg Glu Ala Gly Val Ile Cys Ala Glu Ser Thr Asp Leu Lys Gly Asp
2585                2590                2595                2600

GAA AAA AAT AAT ATT GTG TTA GGT AGC CAA AAA GAT AAT AAC TTA TCG      4439
Glu Lys Asn Asn Ile Val Leu Gly Ser Gln Lys Asp Asn Asn Leu Ser
                2605                2610                2615

GGT AGT GCA GGT GAT GAT CTA CTT ATC GGC GGA GAG GGT AAT GAT ACG      4487
Gly Ser Ala Gly Asp Asp Leu Leu Ile Gly Gly Glu Gly Asn Asp Thr
            2620                2625                2630

TTA AAA GGC AGC TAC GGT GCA GAC ACC TAT ATC TTT AGC AAA GGG CAT      4535
Leu Lys Gly Ser Tyr Gly Ala Asp Thr Tyr Ile Phe Ser Lys Gly His
        2635                2640                2645

GGA CAA GAT GTA ATT TAT GAA TAT TCC GAC AGT GCA AAC TCT AAA AAA      4583
Gly Gln Asp Val Ile Tyr Glu Tyr Ser Asp Ser Ala Asn Ser Lys Lys
    2650                2655                2660

GAT ATT GAT ACC TTA AAA TTT ACC GAT GTG AAT TAT GCG GAA GTG AAG      4631
Asp Ile Asp Thr Leu Lys Phe Thr Asp Val Asn Tyr Ala Glu Val Lys
2665                2670                2675                2680
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TTT CGA CGA GTA GAT AAT GAC TTA ATG TTA TTC GGT TAT CAT GAT ACG      4679
Phe Arg Arg Val Asp Asn Asp Leu Met Leu Phe Gly Tyr His Asp Thr
                2685                2690                2695

GAT TCG GTC ACG GTA AAA TCC TTC TAC AGC CAT GTA GAT TAT CAA TTT      4727
Asp Ser Val Thr Val Lys Ser Phe Tyr Ser His Val Asp Tyr Gln Phe
            2700                2705                2710

GAC AAA TTG GAG TTT GCT GAC CGC AGT ATA ACT CGC GAT GAA CTG ATT      4775
Asp Lys Leu Glu Phe Ala Asp Arg Ser Ile Thr Arg Asp Glu Leu Ile
        2715                2720                2725

AAA GCA GGG CTT CAT CTA TAC GGC ACC GAT GGC AAT GAT GAT ATA AAG      4823
Lys Ala Gly Leu His Leu Tyr Gly Thr Asp Gly Asn Asp Asp Ile Lys
    2730                2735                2740

GAT CAT GCG GAT TGG GAC AGC ATT GTG GAA GGC GGC AAA GGC AAC GAT      4871
Asp His Ala Asp Trp Asp Ser Ile Val Glu Gly Gly Lys Gly Asn Asp
2745                2750                2755                2760

ATT CTA AGA GGT GGC TAC GGT GCG GAC ACC TAT ATC TTT AGC AAA GGA      4919
Ile Leu Arg Gly Gly Tyr Gly Ala Asp Thr Tyr Ile Phe Ser Lys Gly
                2765                2770                2775

CAC GGA CAG GAT ATC GTT TAT GAA GAT ACC AAT AAT GAT AAC CGA GCA      4967
His Gly Gln Asp Ile Val Tyr Glu Asp Thr Asn Asn Asp Asn Arg Ala
            2780                2785                2790

AGA GAT ATC GAC ACC TTA ACA TTT ACT GAT GTG AAT TAT GCG GAA GTG      5015
Arg Asp Ile Asp Thr Leu Thr Phe Thr Asp Val Asn Tyr Ala Glu Val
        2795                2800                2805

AAA TTC CGA CGA GTA GAT AAT GAC TTA ATG TTA TTC GGT TAT CAT GAT      5063
Lys Phe Arg Arg Val Asp Asn Asp Leu Met Leu Phe Gly Tyr His Asp
    2810                2815                2820

ACG GAT TCG GTC ACG ATA AAA TCC TTC TAC AAC CAT GTA GAT TAT CAA      5111
Thr Asp Ser Val Thr Ile Lys Ser Phe Tyr Asn His Val Asp Tyr Gln
2825                2830                2835                2840

TGT GAC AAA TTG GAC TTT GCT GAC CGC AGT ATA ACT CGT GAT GAA CTA      5159
Cys Asp Lys Leu Asp Phe Ala Asp Arg Ser Ile Thr Arg Asp Glu Leu
                2845                2850                2855

GGT AAA CAA GGT ATG GCA TTA TTT GGC ACT GAC GGC GAT GAT AAT ATC      5207
Gly Lys Gln Gly Met Ala Leu Phe Gly Thr Asp Gly Asp Asp Asn Ile
            2860                2865                2870

AAC GAC TGG GGA CGT AAC TCG GTG ATT GAT GCC GGT GCG GGT AAT GAT      5255
Asn Asp Trp Gly Arg Asn Ser Val Ile Asp Ala Gly Ala Gly Asn Asp
        2875                2880                2885

ACG GTT AAT GGC GGT AAT GGC GAT GAC ACC CTC ATC GGC GGC AAA GGT      5303
Thr Val Asn Gly Gly Asn Gly Asp Asp Thr Leu Ile Gly Gly Lys Gly
    2890                2895                2900

AAT GAT ATT CTA AGA GGT GGC TAC GGT GCG GAC ACC TAT ATC TTT AGC      5351
Asn Asp Ile Leu Arg Gly Gly Tyr Gly Ala Asp Thr Tyr Ile Phe Ser
2905                2910                2915                2920

AAA GGA CAC GGA CAG GAT ATC GTT TAT GAA GAT ACC AAT AAT GAT AAC      5399
Lys Gly His Gly Gln Asp Ile Val Tyr Glu Asp Thr Asn Asn Asp Asn
                2925                2930                2935

CGC GCA AGA GAT ATC GAC ACC TTA AAA TTT ACT GAT ATT AAT TTA TCC      5447
Arg Ala Arg Asp Ile Asp Thr Leu Lys Phe Thr Asp Ile Asn Leu Ser
            2940                2945                2950
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GAA CTT TGG TTT AGC CGA GAA AAT AAC GAT TTG ATT ATT AAA TCA TTA      5495
Glu Leu Trp Phe Ser Arg Glu Asn Asn Asp Leu Ile Ile Lys Ser Leu
        2955                2960                2965

TTA AGT GAG GAT AAA GTC ACG GTT CAA AAT TGG TAT TCA CAC CAA GAT      5543
Leu Ser Glu Asp Lys Val Thr Val Gln Asn Trp Tyr Ser His Gln Asp
    2970                2975                2980

CAT AAA ATA GAA AAT ATT CGT TTA TCG AAT GAG CAA ATG TTG GTG AGC      5591
His Lys Ile Glu Asn Ile Arg Leu Ser Asn Glu Gln Met Leu Val Ser
2985                2990                2995                3000

ACT CAG GTG GAG AAG ATG GTT GAG TCG ATG GCC GGC TTT GCT CAG AAG      5639
Thr Gln Val Glu Lys Met Val Glu Ser Met Ala Gly Phe Ala Gln Lys
                3005                3010                3015

CAC GGA GGA GAG ATA TCT CTT CTG TCG CCT GAA GAG GTA AAA CAA TAT      5687
His Gly Gly Glu Ile Ser Leu Leu Ser Pro Glu Glu Val Lys Gln Tyr
            3020                3025                3030

ATC AAT AGC TTA ACA GCT GCT TTA TAA CATACGAAAG AAATCGGCAC            5734
Ile Asn Ser Leu Thr Ala Ala Leu  *
        3035                3040

AGTTTTTGTG AACTGTGCCG ATTTGATTTT AGTGTAAGAA TATAGCCTGA TTTTAAGAAA    5794

TTTACTCTTG GCTAATAACT ATTTCCCATT TTATAAGTTA TTGACGGATG GTTTTATCAA    5854

ATATGAGATC AAATCTTATT TTAAATTCGC TTTCCATTAA GCGATATTGA TCTTTTAAGT    5914

TTGGGGCCGC ATGAGTTTGG AACCGATACC ACTCATTGTG GGAATCAATA CACAATACGC    5974

TGTAATCGGA CTCTTGCAGT TCATAATAAT GCTTTCTCTC CGTTAATTCT TCTTGCGTAT    6034

ATGGCGAGAG ATTAAAGCTG AATGGCTGGT TCGCACTAAC AAACAGGTTC TCCGATTTCA    6094

GATATTCACA ACCGTAATGG CTACCGGTTT CCTGCGGTTT TACATAATTG GTATGATTTT    6154

GTTTAGCTGT TATACGGTAG ATGCCTAATT GTGGTAAATT GCGTGTGTCA ATATAGCTTT    6214

CTTGTTCTCC GTAACCGAAA TACTCAATGG CGTTTTCTGT TTTAGCTAAG AAGAAACGTA    6274

AGCCGAAGCG GGGTAAATAC GGTAATTCGA TCGGGCGAAT AGCGTTAATT TCAACCGAAA    6334

GTTGTCCGTC ATTGAAGATA CGATAACGAA TATCCAGTGT TAAAATGCGA CCGCGAGAAA    6394

TTGACACAAT TGCAGATTTT ACTGAAAATT CGACCGCTTG TTCGCTTTGC TGCCACTGAA    6454

TTTCATACGC TCTGGTATAG GCTTTATCGT AGCCGGCATT TTGGCACGCC TCACGAATGA    6514

GGCGATCATT GTCGGTTGGC GCACGCCAAA TATTAAAATC TAACGATTGT TGGATAATCG    6574

CTTTACCGGC TTTTTCAATA CGGGTGAAAA TCCCTTTCTG TTTATCTAAT TGATAACTAA    6634

ATTGACCGTT GTGTACGTTA ATGTGGAAGC GATCTTCTTG TACTTCAAAT GCACTGTTCT    6694

CAATTGTGAA TTGTGGTAAT ACTAATTTAT TTTCGCTAAA TAAATTGAGC TGCTCGAAGC    6754

CAAGTGAATG TGCTTCGTCT AATAATTCGA CCGCGGTATT TAAGCGATAA TTTAAATTCA    6814

GTAGCCATAA ATGCCCGTTA TTTTTTGGTA ACTCAATCGG TAATACTACG CTGCCGTGCG    6874

GTTGGCAAGA AACGGATAAA TTCCCACCGC TTGTCACCAC GCCGTTTTCG ACAAATTCGT    6934

AATCAATCGT TAAATAATCG GCAAGATCAG TGAAATCCAA GTAGTTGTGG ATCACAATTT    6994

GGTTATCGAT                                                           7004
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(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1383 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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Met Ser Asp Asn Ala Phe Phe Val Ile Glu Glu Ser Gly Lys Arg Tyr
 1               5                  10                  15

Ile Glu Asn Phe Gly Ile Glu Pro Leu Gly Lys Gln Glu Asp Phe Asp
            20                  25                  30

Phe Val Gly Gly Phe Trp Ser Asn Leu Val Asn Arg Gly Leu Glu Ser
        35                  40                  45

Ile Ile Asp Pro Ser Gly Ile Gly Gly Thr Val Asn Leu Asn Phe Thr
    50                  55                  60

Gly Glu Val Glu Thr Tyr Thr Leu Asp Glu Thr Arg Phe Lys Ala Glu
65                  70                  75                  80

Ala Ala Lys Lys Ser His Trp Ser Leu Val Asn Ala Ala Lys Val Tyr
                85                  90                  95

Gly Gly Leu Asp Gln Ile Ile Lys Lys Leu Trp Asp Ser Gly Ser Ile
            100                 105                 110

Lys His Leu Tyr Gln Asp Lys Asp Thr Gly Lys Leu Lys Pro Ile Ile
        115                 120                 125

Tyr Gly Thr Ala Gly Asn Asp Ser Lys Ile Glu Gly Thr Lys Ile Thr
    130                 135                 140

Arg Arg Ile Ala Gly Lys Glu Val Thr Leu Asp Ile Ala Asn Gln Lys
145                 150                 155                 160

Ile Glu Lys Gly Val Leu Glu Lys Leu Gly Leu Ser Val Ser Gly Ser
                165                 170                 175

Asp Ile Ile Lys Leu Leu Phe Gly Ala Leu Thr Pro Thr Leu Asn Arg
            180                 185                 190

Met Leu Leu Ser Gln Leu Ile Gln Ser Phe Ser Asp Ser Leu Ala Lys
        195                 200                 205

Leu Asp Asn Pro Leu Ala Pro Tyr Thr Lys Asn Gly Val Val Tyr Val
    210                 215                 220

Thr Gly Lys Gly Asn Asp Val Leu Lys Gly Thr Glu His Glu Asp Leu
225                 230                 235                 240

Phe Leu Gly Gly Glu Gly Asn Asp Thr Tyr Tyr Ala Arg Val Gly Asp
                245                 250                 255

Thr Ile Glu Asp Ala Asp Gly Lys Gly Lys Val Tyr Phe Val Arg Glu
            260                 265                 270

Lys Gly Val Pro Lys Ala Asp Pro Lys Arg Val Glu Phe Ser Glu Tyr
        275                 280                 285

Ile Thr Lys Glu Glu Ile Lys Glu Val Glu Lys Gly Leu Leu Thr Tyr
    290                 295                 300

Ala Val Leu Glu Asn Tyr Asn Trp Glu Glu Lys Thr Ala Thr Phe Ala
305                 310                 315                 320
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His Ala Thr Met Leu Asn Glu Leu Phe Thr Asp Tyr Thr Asn Tyr Arg
                325                 330                 335

Tyr Glu Val Lys Gly Leu Lys Leu Pro Ala Val Lys Lys Leu Lys Ser
            340                 345                 350

Pro Leu Val Glu Phe Thr Ala Asp Leu Leu Thr Val Thr Pro Ile Asp
        355                 360                 365

Glu Asn Gly Lys Ala Leu Ser Glu Lys Ser Ile Thr Val Lys Asn Phe
    370                 375                 380

Lys Asn Gly Asp Leu Gly Ile Arg Leu Leu Asp Pro Asn Ser Tyr Tyr
385                 390                 395                 400

Tyr Phe Leu Glu Gly Gln Asp Thr Gly Phe Tyr Gly Pro Ala Phe Tyr
                405                 410                 415

Ile Glu Arg Lys Asn Gly Gly Gly Ser Lys Asn Asn Ser Ser Gly Ala
            420                 425                 430

Gly Asn Ser Lys Asp Trp Gly Gly Asn Gly His Gly Asn His Arg Asn
        435                 440                 445

Asn Ala Ser Asp Leu Asn Lys Pro Asp Gly Asn Asn Gly Asn Asn Gln
    450                 455                 460

Asn Asn Gly Ser Asn Gln Asp Asn His Ser Asp Val Asn Ala Pro Asn
465                 470                 475                 480

Asn Pro Gly Arg Asn Tyr Asp Ile Tyr Asp Pro Leu Ala Leu Asp Leu
                485                 490                 495

Asp Gly Asp Gly Leu Glu Thr Val Ser Met Asn Gly Arg Gln Gly Ala
            500                 505                 510

Leu Phe Asp His Glu Gly Lys Gly Ile Arg Thr Ala Thr Gly Trp Leu
        515                 520                 525

Ala Ala Asp Asp Gly Phe Leu Val Leu Asp Arg Asn Gln Asp Gly Ile
    530                 535                 540

Ile Asn Asp Ile Ser Glu Leu Phe Ser Asn Lys Asn Gln Leu Ser Asp
545                 550                 555                 560

Gly Ser Ile Ser Ala His Gly Phe Ala Thr Leu Ala Asp Leu Asp Thr
                565                 570                 575

Asn Gln Asp Gln Arg Ile Asp Gln Asn Asp Lys Leu Phe Ser Lys Leu
            580                 585                 590

Gln Ile Trp Arg Asp Leu Asn Gln Asn Gly Phe Ser Glu Ala Asn Glu
        595                 600                 605

Leu Phe Ser Leu Glu Ser Leu Asn Ile Lys Ser Leu His Thr Ala Tyr
    610                 615                 620

Glu Glu Arg Asn Asp Phe Leu Ala Gly Asn Asn Ile Leu Ala Gln Leu
625                 630                 635                 640

Gly Lys Tyr Glu Lys Thr Asp Gly Thr Phe Gly Gln Met Gly Asp Leu
                645                 650                 655

Asn Phe Ser Phe Asn Pro Phe Tyr Ser Arg Phe Thr Glu Ala Leu Asn
            660                 665                 670

Leu Thr Glu Gln Gln Arg Arg Thr Ile Asn Leu Thr Gly Thr Gly Arg
        675                 680                 685
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Val Arg Asp Leu Arg Glu Ala Ala Ala Leu Ser Glu Glu Leu Ala Ala
690                 695                 700

Leu Leu Gln Gln Tyr Thr Lys Gly Ser Asp Phe Gln Ala Gln Arg Glu
705                 710                 715                 720

Leu Leu Pro Ala Ile Leu Asp Lys Trp Ala Ala Thr Asp Leu Gln Tyr
                725                 730                 735

Gln His Tyr Asp Lys Thr Leu Leu Lys Thr Val Glu Ser Thr Asp Ser
            740                 745                 750

Ser Ala Ser Val Val Arg Val Thr Pro Ser Gln Leu Ser Ser Ile Arg
        755                 760                 765

Asn Val Lys His Asp Pro Thr Val Met Gln Asn Cys Glu Gln Ser Lys
    770                 775                 780

Ala Lys Ile Ala Thr Leu Asn Ser Leu Tyr Gly Leu Asn Ile Asp Gln
785                 790                 795                 800

Leu Tyr Tyr Thr Thr Asp Lys Asp Ile Arg Tyr Ile Thr Asp Lys Val
                805                 810                 815

Asn Asn Met Tyr Gln Thr Thr Gly Glu Leu Gly Tyr Arg Ser Leu Leu
            820                 825                 830

Leu Gln Thr Arg Val Lys Lys Tyr Val Tyr Ser Val Asn Ala Lys Gln
        835                 840                 845

Phe Glu Gly Lys Trp Val Ala Asp Tyr Ser Arg Thr Glu Ala Leu Phe
    850                 855                 860

Asn Ser Thr Tyr Lys Gln Ser Pro Glu Asn Val Leu Tyr Asp Leu Arg
865                 870                 875                 880

Glu Tyr Leu Ser Phe Tyr Asn Asp Pro Thr Glu Trp Lys Glu Gly Leu
                885                 890                 895

Leu Leu Leu Ser Arg Tyr Ile Asp Tyr Ala Lys Ala Gln Gly Phe Tyr
            900                 905                 910

Glu Asn Trp Ala Ala Thr Ser Asn Leu Thr Ile Ala Arg Leu Arg Glu
        915                 920                 925

Ala Gly Val Ile Cys Ala Glu Ser Thr Asp Leu Lys Gly Asp Glu Lys
    930                 935                 940

Asn Asn Ile Val Leu Gly Ser Gln Lys Asp Asn Asn Leu Ser Gly Ser
945                 950                 955                 960

Ala Gly Asp Asp Leu Leu Ile Gly Gly Glu Gly Asn Asp Thr Leu Lys
                965                 970                 975

Gly Ser Tyr Gly Ala Asp Thr Tyr Ile Phe Ser Lys Gly His Gly Gln
            980                 985                 990

Asp Val Ile Tyr Glu Tyr Ser Asp Ser Ala Asn Ser Lys Lys Asp Ile
        995                 1000                1005

Asp Thr Leu Lys Phe Thr Asp Val Asn Tyr Ala Glu Val Lys Phe Arg
    1010                1015                1020

Arg Val Asp Asn Asp Leu Met Leu Phe Gly Tyr His Asp Thr Asp Ser
1025                1030                1035                1040

Val Thr Val Lys Ser Phe Tyr Ser His Val Asp Tyr Gln Phe Asp Lys
                1045                1050                1055
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Leu Glu Phe Ala Asp Arg Ser Ile Thr Arg Asp Glu Leu Ile Lys Ala
1060 1065 1070

Gly Leu His Leu Tyr Gly Thr Asp Gly Asn Asp Asp Ile Lys Asp His
1075 1080 1085

Ala Asp Trp Asp Ser Ile Val Glu Gly Gly Lys Gly Asn Asp Ile Leu
1090 1095 1100

Arg Gly Gly Tyr Gly Ala Asp Thr Tyr Ile Phe Ser Lys Gly His Gly
1105 1110 1115 1120

Gln Asp Ile Val Tyr Glu Asp Thr Asn Asn Asp Asn Arg Ala Arg Asp
1125 1130 1135

Ile Asp Thr Leu Thr Phe Thr Asp Val Asn Tyr Ala Glu Val Lys Phe
1140 1145 1150

Arg Arg Val Asp Asn Asp Leu Met Leu Phe Gly Tyr His Asp Thr Asp
1155 1160 1165

Ser Val Thr Ile Lys Ser Phe Tyr Asn His Val Asp Tyr Gln Cys Asp
1170 1175 1180

Lys Leu Asp Phe Ala Asp Arg Ser Ile Thr Arg Asp Glu Leu Gly Lys
1185 1190 1195 1200

Gln Gly Met Ala Leu Phe Gly Thr Asp Gly Asp Asp Asn Ile Asn Asp
1205 1210 1215

Trp Gly Arg Asn Ser Val Ile Asp Ala Gly Ala Gly Asn Asp Thr Val
1220 1225 1230

Asn Gly Gly Asn Gly Asp Asp Thr Leu Ile Gly Gly Lys Gly Asn Asp
1235 1240 1245

Ile Leu Arg Gly Gly Tyr Gly Ala Asp Thr Tyr Ile Phe Ser Lys Gly
1250 1255 1260

His Gly Gln Asp Ile Val Tyr Glu Asp Thr Asn Asn Asp Asn Arg Ala
1265 1270 1275 1280

Arg Asp Ile Asp Thr Leu Lys Phe Thr Asp Ile Asn Leu Ser Glu Leu
1285 1290 1295

Trp Phe Ser Arg Glu Asn Asn Asp Leu Ile Ile Lys Ser Leu Leu Ser
1300 1305 1310

Glu Asp Lys Val Thr Val Gln Asn Trp Tyr Ser His Gln Asp His Lys
1315 1320 1325

Ile Glu Asn Ile Arg Leu Ser Asn Glu Gln Met Leu Val Ser Thr Gln
1330 1335 1340

Val Glu Lys Met Val Glu Ser Met Ala Gly Phe Ala Gln Lys His Gly
1345 1350 1355 1360

Gly Glu Ile Ser Leu Leu Ser Pro Glu Glu Val Lys Gln Tyr Ile Asn
1365 1370 1375

Ser Leu Thr Ala Ala Leu *
1380

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6736 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Actinobacillus pleuropneumoniae
(B) STRAIN: 4074 (serotype 1 reference strain)

(vii) IMMEDIATE SOURCE:
(B) CLONE: pROK7

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1132..6549
(C) IDENTIFICATION METHOD: experimental
(D) OTHER INFORMATION:/codon_start= 1132
/function= "RTX toxin"
/product= "ApxIV"
/evidence= EXPERIMENTAL
/gene= "ApxIV_v1"

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:639..1178
(D) OTHER INFORMATION:/codon_start= 639
/function= "unknown"
/product= "ORF1"
/gene= "orf1"

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..453
(D) OTHER INFORMATION:/partial
/product= "Met-G"
/gene= "mrp"
/standard_name= "mrp"
/label= mrp

(ix) FEATURE:
(A) NAME/KEY: -10_signal
(B) LOCATION:617..623
(D) OTHER INFORMATION:/standard_name= "-10"
/label= -10_s

(ix) FEATURE:
(A) NAME/KEY: -35_signal
(B) LOCATION:594..599
(D) OTHER INFORMATION:/standard_name= "-35_s"
/label= -35_s

(ix) FEATURE:
(A) NAME/KEY: promoter
(B) LOCATION:454..1131
(D) OTHER INFORMATION:/function= "Promoter"
/standard_name= "promoter ApxIV"
/label= promoter

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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ATC GAT ATG CCG CCG GGT ACG GGC GAT ATC CAA CTT ACT CTT TCG CAA        48
Ile Asp Met Pro Pro Gly Thr Gly Asp Ile Gln Leu Thr Leu Ser Gln
  1               5                  10                  15

CAA ATT CCG GTT ACC GGT GCG GTG GTG GTA ACC ACT CCG CAA GAT ATT        96
Gln Ile Pro Val Thr Gly Ala Val Val Val Thr Thr Pro Gln Asp Ile
            20                  25                  30

GCG TTA TTA GAT GCG GTG AAA GGT ATT TCA ATG TTC CAA AAA GTG TCG       144
Ala Leu Leu Asp Ala Val Lys Gly Ile Ser Met Phe Gln Lys Val Ser
        35                  40                  45

GTA CCG GTC TTA GGT ATC ATT GAA AAT ATG AGC GTA CAT ATC TGC CAA       192
Val Pro Val Leu Gly Ile Ile Glu Asn Met Ser Val His Ile Cys Gln
    50                  55                  60
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AAT TGC GGT CAC CAC GAA GAT ATT TTC GGC ACC GGC GGT GCG GAG AAA        240
Asn Cys Gly His His Glu Asp Ile Phe Gly Thr Gly Gly Ala Glu Lys
 65                  70                  75                  80

GTG GCG AAG AAA TAC GGT ACT AAA GTA TTA GGA CAA ATG CCG TTG CAT        288
Val Ala Lys Lys Tyr Gly Thr Lys Val Leu Gly Gln Met Pro Leu His
                 85                  90                  95

ATT CGC TTA CGT CAA GAT TTG GAT GCC GGC ACA CCG ACC GTC GTT GCG        336
Ile Arg Leu Arg Gln Asp Leu Asp Ala Gly Thr Pro Thr Val Val Ala
            100                 105                 110

GCA CCG GAA CAC GAA ACC AGC CGA GCC TAT ATT GAA TTA GCG GCA AAA        384
Ala Pro Glu His Glu Thr Ser Arg Ala Tyr Ile Glu Leu Ala Ala Lys
        115                 120                 125

GTC GCT TCG GAA TTA TAC TGG CAA GGT TCG GTT ATC CCG TCT GAA ATT        432
Val Ala Ser Glu Leu Tyr Trp Gln Gly Ser Val Ile Pro Ser Glu Ile
    130                 135                 140

ATG ATT CGT GAA GTA AAA TAA GTTTTAATAA CCACGAAAAC ACAAAGAACA           483
Met Ile Arg Glu Val Lys  *
145                 150

CAAGCGGTAG AATTTGCAGA AAAATTTGCA AATCCTACCG CTTTTTTATT AGTACGATTC      543

GCTGTTGGAC TGCTATTTGA TTTGGTTTGT CAGGATATTA TGTTATTGTA ATGAAATGTT      603

AGTGAATTAT TTTTATTAAT TTGAAAGGAA ACAAAATGAA AATAAAAAAA CGTTACATTG      663

CGCTGTTGGT CTTAGGTGTC GTTATCAGCT ATGCCTGGTA TCAAAATTAT CAATGGGAAC      723

AGCTGATGTT AAGCGGTTAT TGTGAAAAGG ACGGAAGTTA TTTTGATGAT AGGCATACGA      783

AGCAAGAACT GATTGATAGG GCAATTAACT ATATGCTGGA GCATCAATCT AAAAAAACAT      843

ACGATGCTTA TACTGATGAA CCTTTAGAAA TAAAACCATA TTTAACAATA GAGGAATTTA      903

AAAAACTCAA TCCAAATTGT TGTGAAATTA CCTCATGGCC AGCAGATGCA GTTCCACAAG      963

ATTGGGATGT TCGTGTGGAA GGTAAGGCAT ATAGGTATGT AATCGTAAAA TATTTAAGAA     1023

CCTTAGCAAA TAGAGAACCT GAACGATGGG AAACTAGTAT TGTTTTTGAT AATTGCGGCA     1083

ATCCTAAAAG AGCAAGCTAC TTATATTATT TAAAGAGAGA AATTTATT ATG ACA AAA      1140
                                                 Met Thr Lys
                                                   1

TTA ACT ATG CAA GAT GTG ACC AAT TTA TAT TTA TAT AAA ACG AAA ACT       1188
Leu Thr Met Gln Asp Val Thr Asn Leu Tyr Leu Tyr Lys Thr Lys Thr
      5                  10                  15

CTA CCT AAA GAT AGA TTG GAT GAT TCA CTT ATT TCT GAA ATA GGA AAA       1236
Leu Pro Lys Asp Arg Leu Asp Asp Ser Leu Ile Ser Glu Ile Gly Lys
 20                  25                  30                  35

GGA GAT GAT GAT ATT GAT AGA AAA GAA TTT ATG GTG GGG CCG GGA CGT       1284
Gly Asp Asp Asp Ile Asp Arg Lys Glu Phe Met Val Gly Pro Gly Arg
                 40                  45                  50

TTT GTG ACC GCT GAT AAC TTT AGC GTT GTA AGA GAT TTT TTT AAT GCT       1332
Phe Val Thr Ala Asp Asn Phe Ser Val Val Arg Asp Phe Phe Asn Ala
            55                  60                  65

GGG AAA TCA CGC ATT ATT GCG CCG CAA GTC CCG CCT ATT CGT TCA CAG       1380
Gly Lys Ser Arg Ile Ile Ala Pro Gln Val Pro Pro Ile Arg Ser Gln
        70                  75                  80

CAG GAA AAA ATC TTG GTC GGT TTA AAA CCG GGC AAA TAT TCC AAA GCG       1428
Gln Glu Lys Ile Leu Val Gly Leu Lys Pro Gly Lys Tyr Ser Lys Ala
 85                  90                  95

CAG ATA TTG GAA ATG CTG GGT TAT ACG AAA GGC GGA GAA GTG GTA AAT       1476
Gln Ile Leu Glu Met Leu Gly Tyr Thr Lys Gly Gly Glu Val Val Asn
100                 105                 110                 115

GGC ATG TTT GCC GGT GAA GTC CAG ACA TTA GGC TTT TAT GAC GAT GGC       1524
Gly Met Phe Ala Gly Glu Val Gln Thr Leu Gly Phe Tyr Asp Asp Gly
                120                 125                 130

AAA GGG GAT TTA CTC GAA CGC GCC TAT ATC TGG AAT ACC ACA GGA TTT       1572
Lys Gly Asp Leu Leu Glu Arg Ala Tyr Ile Trp Asn Thr Thr Gly Phe
            135                 140                 145

AAA ATG AGC GAC AAT GCC TTT TTT GTT ATA GAA GAA TCA GGC AAA CGC       1620
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Lys Met Ser Asp Asn Ala Phe Phe Val Ile Glu Glu Ser Gly Lys Arg
        150                 155                 160

TAT ATT GAA AAC TTT GGT ATT GAA CCT CTT GGT AAG CAA GAA GAT TTT   1668
Tyr Ile Glu Asn Phe Gly Ile Glu Pro Leu Gly Lys Gln Glu Asp Phe
    165                 170                 175

GAT TTT GTC GGC GGC TTT TGG TCT AAC TTA GTG AAT CGT GGT TTG GAA   1716
Asp Phe Val Gly Gly Phe Trp Ser Asn Leu Val Asn Arg Gly Leu Glu
180                 185                 190                 195

AGT ATT ATC GAC CCA TCC GGT ATC GGT GGA ACG GTA AAC CTT AAC TTT   1764
Ser Ile Ile Asp Pro Ser Gly Ile Gly Gly Thr Val Asn Leu Asn Phe
                200                 205                 210

ACC GGC GAG GTG GAA ACC TAC ACG TTA GAC GAA ACA AGG TTT AAA GCG   1812
Thr Gly Glu Val Glu Thr Tyr Thr Leu Asp Glu Thr Arg Phe Lys Ala
            215                 220                 225

GAA GCG GCG AAG AAA AGC CAT TGG AGT TTA GTG AAT GCG GCG AAA GTA   1860
Glu Ala Ala Lys Lys Ser His Trp Ser Leu Val Asn Ala Ala Lys Val
        230                 235                 240

TAC GGC GGT TTA GAC CAA ATT ATT AAA AAA CTA TGG GAC AGT GGC TCA   1908
Tyr Gly Gly Leu Asp Gln Ile Ile Lys Lys Leu Trp Asp Ser Gly Ser
    245                 250                 255

ATT AAG CAT TTA TAT CAA GAT AAA GAT ACG GGC AAA TTA AAA CCG ATT   1956
Ile Lys His Leu Tyr Gln Asp Lys Asp Thr Gly Lys Leu Lys Pro Ile
260                 265                 270                 275

ATT TAC GGC ACG GCC GGC AAC GAC AGT AAG ATT GAA GGC ACT AAA ATC   2004
Ile Tyr Gly Thr Ala Gly Asn Asp Ser Lys Ile Glu Gly Thr Lys Ile
                280                 285                 290

ACC CGT AGG ATT GCG GGT AAA GAA GTT ACG CTT GAT ATT GCC AAT CAG   2052
Thr Arg Arg Ile Ala Gly Lys Glu Val Thr Leu Asp Ile Ala Asn Gln
            295                 300                 305

AAA ATT GAA AAA GGC GTG TTA GAG AAA TTG GGG CTG TCT GTT AGT GGT   2100
Lys Ile Glu Lys Gly Val Leu Glu Lys Leu Gly Leu Ser Val Ser Gly
        310                 315                 320

TCG GAT ATC ATT AAA TTG TTG TTT GGA GCA TTG ACT CCA ACT TTA AAT   2148
Ser Asp Ile Ile Lys Leu Leu Phe Gly Ala Leu Thr Pro Thr Leu Asn
    325                 330                 335

AGA ATG TTG CTA TCA CAA CTT ATC CAG TCT TTT TCC GAT AGC TTG GCT   2196
Arg Met Leu Leu Ser Gln Leu Ile Gln Ser Phe Ser Asp Ser Leu Ala
340                 345                 350                 355

AAA CTT GAT AAT CCC TTA GCC CCT TAC ACT AAA AAT GGC GTG GTT TAT   2244
Lys Leu Asp Asn Pro Leu Ala Pro Tyr Thr Lys Asn Gly Val Val Tyr
                360                 365                 370

GTC ACC GGC AAA GGG AAT GAT GTG CTT AAA GGA ACT GAA CAT GAG GAT   2292
Val Thr Gly Lys Gly Asn Asp Val Leu Lys Gly Thr Glu His Glu Asp
            375                 380                 385

TTG TTT CTC GGT GGT GAG GGG AAT GAT ACT TAT TAT GCG AGA GTA GGC   2340
Leu Phe Leu Gly Gly Glu Gly Asn Asp Thr Tyr Tyr Ala Arg Val Gly
        390                 395                 400

GAT ACA ATT GAA GAC GCC GAC GGC AAA GGT AAA GTC TAT TTT GTG AGA   2388
Asp Thr Ile Glu Asp Ala Asp Gly Lys Gly Lys Val Tyr Phe Val Arg
    405                 410                 415

GAA AAA GGG GTA CCT AAG GCG GAT CCT AAG CGG GTA GAG TTT AGC GAG   2436
Glu Lys Gly Val Pro Lys Ala Asp Pro Lys Arg Val Glu Phe Ser Glu
420                 425                 430                 435

TAC ATA ACG AAA GAA GAA ATA AAA GAG GTT GAA AAG GGG TTA TTA ACT   2484
Tyr Ile Thr Lys Glu Glu Ile Lys Glu Val Glu Lys Gly Leu Leu Thr
                440                 445                 450

TAC GCA GTT TTA GAA AAT TAT AAT TGG GAA GAG AAA ACG GCG ACT TTC   2532
Tyr Ala Val Leu Glu Asn Tyr Asn Trp Glu Glu Lys Thr Ala Thr Phe
            455                 460                 465

GCT CAT GCG ACT ATG CTT AAT GAG CTT TTT ACT GAT TAT ACT AAT TAT   2580
Ala His Ala Thr Met Leu Asn Glu Leu Phe Thr Asp Tyr Thr Asn Tyr
        470                 475                 480

CGT TAT GAA GTT AAA GGA CTA AAA TTG CCC GCC GTT AAA AAG TTA AAA   2628
Arg Tyr Glu Val Lys Gly Leu Lys Leu Pro Ala Val Lys Lys Leu Lys
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     485                 490                 495

AGT CCG TTG GTG GAG TTT ACA GCT GAT TTA TTA ACT GTT ACG CCT ATT      2676
Ser Pro Leu Val Glu Phe Thr Ala Asp Leu Leu Thr Val Thr Pro Ile
500                 505                 510                 515

GAC GAA AAC GGA AAA GCA CTT AGC GAA AAA AGT ATT ACG GTT AAA AAT      2724
Asp Glu Asn Gly Lys Ala Leu Ser Glu Lys Ser Ile Thr Val Lys Asn
                520                 525                 530

TTT AAA AAT GGT GAT TTA GGA ATA AGG TTG TTG GAT CCT AAT AGC TAT      2772
Phe Lys Asn Gly Asp Leu Gly Ile Arg Leu Leu Asp Pro Asn Ser Tyr
            535                 540                 545

TAT TAT TTC CTT GAA GGC CAA GAT ACG GGT TTT TAT GGT CCT GCT TTT      2820
Tyr Tyr Phe Leu Glu Gly Gln Asp Thr Gly Phe Tyr Gly Pro Ala Phe
        550                 555                 560

TAT ATT GAA CGA AAA AAC GGT GGC GGC GCT AAA AAT AAC TCG TCG GGA      2868
Tyr Ile Glu Arg Lys Asn Gly Gly Gly Ala Lys Asn Asn Ser Ser Gly
    565                 570                 575

GCA GGA AAT AGC AAA GAT TGG GGC GGG AAC GGG CAT GGA AAT CAC CGA      2916
Ala Gly Asn Ser Lys Asp Trp Gly Gly Asn Gly His Gly Asn His Arg
580                 585                 590                 595

AAT AAT GCC TCC GAC CTG AAT AAA CCG GAC GGA AAT AAT GGG AAT AAC      2964
Asn Asn Ala Ser Asp Leu Asn Lys Pro Asp Gly Asn Asn Gly Asn Asn
                600                 605                 610

CAA AAT AAC GGA AGC AAT CAA GAT AAT CAT AGC GAT GTG AAT GCG CCA      3012
Gln Asn Asn Gly Ser Asn Gln Asp Asn His Ser Asp Val Asn Ala Pro
            615                 620                 625

AAT AAC CCG GGA CGT AAC TAT GAT ATT TAC GAT CCT TTA GCT TTA GAT      3060
Asn Asn Pro Gly Arg Asn Tyr Asp Ile Tyr Asp Pro Leu Ala Leu Asp
        630                 635                 640

TTA GAT GGA GAT GGG CTT GAA ACC GTG TCG ATG AAC GGG CGA CAA GGC      3108
Leu Asp Gly Asp Gly Leu Glu Thr Val Ser Met Asn Gly Arg Gln Gly
    645                 650                 655

GCG TTA TTC GAT CAT GAA GGA AAA GGT ATT CGT ACC GCA ACG GGC TGG      3156
Ala Leu Phe Asp His Glu Gly Lys Gly Ile Arg Thr Ala Thr Gly Trp
660                 665                 670                 675

CTC GCT GCG GAT GAC GGT TTT TTA GTG TTA GAT CGT AAC CAA GAC GGC      3204
Leu Ala Ala Asp Asp Gly Phe Leu Val Leu Asp Arg Asn Gln Asp Gly
                680                 685                 690

ATT ATT AAT GAT ATA AGC GAG TTA TTT AGT AAT AAA AAT CAA CTT TCC      3252
Ile Ile Asn Asp Ile Ser Glu Leu Phe Ser Asn Lys Asn Gln Leu Ser
            695                 700                 705

GAC GGC AGT ATT TCT GCA CAC GGT TTT GCG ACA TTA GCC GAT TTG GAT      3300
Asp Gly Ser Ile Ser Ala His Gly Phe Ala Thr Leu Ala Asp Leu Asp
        710                 715                 720

ACA AAC CAA GAT CAG CGT ATC GAC CAA AAT GAT AAG CTG TTT TCT AAA      3348
Thr Asn Gln Asp Gln Arg Ile Asp Gln Asn Asp Lys Leu Phe Ser Lys
    725                 730                 735

CTC CAA ATT TGG CGG GAT TTA AAT CAA AAC GGT TTT AGT GAA GCG AAT      3396
Leu Gln Ile Trp Arg Asp Leu Asn Gln Asn Gly Phe Ser Glu Ala Asn
740                 745                 750                 755

GAG CTG TTT AGC TTA GAA AGT TTG AAT ATT AAA TCT TTA CAT ACC GCC      3444
Glu Leu Phe Ser Leu Glu Ser Leu Asn Ile Lys Ser Leu His Thr Ala
                760                 765                 770

TAT GAA GAG CGT AAT GAT TTT CTA GCG GGC AAT AAT ATC CTT GCT CAG      3492
Tyr Glu Glu Arg Asn Asp Phe Leu Ala Gly Asn Asn Ile Leu Ala Gln
            775                 780                 785

CTT GGG AAG TAT GAA AAA ACG GAC GGT ACT TTT GCA CAA ATG GGC GAT      3540
Leu Gly Lys Tyr Glu Lys Thr Asp Gly Thr Phe Ala Gln Met Gly Asp
        790                 795                 800

TTA AAT TTC AGT TTT AAC CCG TTT TAT AGC CGA TTT ACC GAA GCG TTA      3588
Leu Asn Phe Ser Phe Asn Pro Phe Tyr Ser Arg Phe Thr Glu Ala Leu
    805                 810                 815

AAT TTA ACC GAG CAA CAA CGT CGC ACA ATT AAT CTA ACC GGC ACC GGT      3636
Asn Leu Thr Glu Gln Gln Arg Arg Thr Ile Asn Leu Thr Gly Thr Gly
820                 825                 830                 835
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CGG GTT CGG GAT TTG CGT GAA GCC GCC GCA CTT TCT GAG GAG TTG GCT      3684
Arg Val Arg Asp Leu Arg Glu Ala Ala Ala Leu Ser Glu Glu Leu Ala
                840                 845                 850

GCT TTA TTA CAA CAG TAC ACT AAG GCC TCC GAT TTT CAG GCA CAA CGA      3732
Ala Leu Leu Gln Gln Tyr Thr Lys Ala Ser Asp Phe Gln Ala Gln Arg
            855                 860                 865

GAA TTA TTG CCT GCC ATT TTA GAT AAA TGG GCG GCA ACG GAT TTA CAG      3780
Glu Leu Leu Pro Ala Ile Leu Asp Lys Trp Ala Ala Thr Asp Leu Gln
        870                 875                 880

TAT CAA CAT TAT GAT AAA ACA TTA CTT AAA ACG GTA GAA AGT ACC GAT      3828
Tyr Gln His Tyr Asp Lys Thr Leu Leu Lys Thr Val Glu Ser Thr Asp
    885                 890                 895

AGT AGT GCT TCT GTC GTT AGA GTC ACG CCT TCT CAA TTA AGT AGT ATA      3876
Ser Ser Ala Ser Val Val Arg Val Thr Pro Ser Gln Leu Ser Ser Ile
900                 905                 910                 915

CGC AAT GCA AAG CAT GAT CCT ACC GTT ATG CAA AAC TTT GAA CAG AGT      3924
Arg Asn Ala Lys His Asp Pro Thr Val Met Gln Asn Phe Glu Gln Ser
                920                 925                 930

AAG GCA AAA ATT GCG ACT TTA AAT TCG CTC TAC GGG TTA AAT ATC GAT      3972
Lys Ala Lys Ile Ala Thr Leu Asn Ser Leu Tyr Gly Leu Asn Ile Asp
            935                 940                 945

CAA CTT TAT TAC ACG ACG GAT AAA GAC ATT CGC TAT ATT ACT GAT AAA      4020
Gln Leu Tyr Tyr Thr Thr Asp Lys Asp Ile Arg Tyr Ile Thr Asp Lys
        950                 955                 960

GTG AAT AAT ATG TAT CAA ACA ACC GTA GAA CTT GCC TAC CGT TCT TTA      4068
Val Asn Asn Met Tyr Gln Thr Thr Val Glu Leu Ala Tyr Arg Ser Leu
    965                 970                 975

CTT TTA CAA ACG CGT TTG AAG AAA TAT GTT TAT AGC GTT AAT GCG AAA      4116
Leu Leu Gln Thr Arg Leu Lys Lys Tyr Val Tyr Ser Val Asn Ala Lys
980                 985                 990                 995

CAA TTC GAA GGG AAA TGG GTA ACC GAT TAT TCT CGT ACT GAA GCC TTA      4164
Gln Phe Glu Gly Lys Trp Val Thr Asp Tyr Ser Arg Thr Glu Ala Leu
                1000                1005                1010

TTT AAC TCT ACT TTT AAA CAA TCG CCT GAA AAT GCA TTA TAT GAT TTA      4212
Phe Asn Ser Thr Phe Lys Gln Ser Pro Glu Asn Ala Leu Tyr Asp Leu
            1015                1020                1025

AGC GAA TAC CTT TCT TTC TTT AAC GAT CCT ACG GAA TGG AAA GAA GGG      4260
Ser Glu Tyr Leu Ser Phe Phe Asn Asp Pro Thr Glu Trp Lys Glu Gly
        1030                1035                1040

CTA TTA CTG TTA AGC CGT TAT ATA GAT TAT GCT AAA GCA CAA GGA TTT      4308
Leu Leu Leu Leu Ser Arg Tyr Ile Asp Tyr Ala Lys Ala Gln Gly Phe
    1045                1050                1055

TAT GAA AAC TGG GCG GCT ACT TCT AAC TTA ACT ATT GCC CGT TTA AGA      4356
Tyr Glu Asn Trp Ala Ala Thr Ser Asn Leu Thr Ile Ala Arg Leu Arg
1060                1065                1070                1075

GAG GCT GGA GTA ATT TTT GCA GAA TCG ACG GAT TTA AAA GGC GAT GAA      4404
Glu Ala Gly Val Ile Phe Ala Glu Ser Thr Asp Leu Lys Gly Asp Glu
                1080                1085                1090

AAA AAT AAT ATT TTG TTA GGT AGC CAA AAA GAT AAT AAC TTA TCG GGT      4452
Lys Asn Asn Ile Leu Leu Gly Ser Gln Lys Asp Asn Asn Leu Ser Gly
            1095                1100                1105

AGT GCA GGT GAT GAT CTA CTT ATC GGC GGA GAG GGT AAT GAT ACG TTA      4500
Ser Ala Gly Asp Asp Leu Leu Ile Gly Gly Glu Gly Asn Asp Thr Leu
        1110                1115                1120

AAA GGC AGC TAC GGT GCA GAC ACC TAT ATC TTT AGC AAA GGA CAC GGA      4548
Lys Gly Ser Tyr Gly Ala Asp Thr Tyr Ile Phe Ser Lys Gly His Gly
    1125                1130                1135

CAG GAT ATC GTT TAT GAA GAT ACC AAT AAT GAT AAC CGC GCA AGA GAT      4596
Gln Asp Ile Val Tyr Glu Asp Thr Asn Asn Asp Asn Arg Ala Arg Asp
1140                1145                1150                1155

ATC GAC ACC TTA AAA TTT ACC GAT GTG AAT TAT GCG GAA GTG AAG TTT      4644
Ile Asp Thr Leu Lys Phe Thr Asp Val Asn Tyr Ala Glu Val Lys Phe
                1160                1165                1170

CGA CGA GTA GAT AAT GAC TTA ATG TTA TTC GGT TAT CAT GAT ACG GAT      4692
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Arg Arg Val Asp Asn Asp Leu Met Leu Phe Gly Tyr His Asp Thr Asp
                1175                1180                1185

TCG GTC ACG GTA AAA TCC TTC TAC AGC CAT GTA GAT TAT CAA TTT GAC      4740
Ser Val Thr Val Lys Ser Phe Tyr Ser His Val Asp Tyr Gln Phe Asp
        1190                1195                1200

AAA TTG GAG TTT GCT GAC CGC AGT ATA ACT CGC GAT GAA CTG ATT AAA      4788
Lys Leu Glu Phe Ala Asp Arg Ser Ile Thr Arg Asp Glu Leu Ile Lys
    1205                1210                1215

GCA GGG CTT CAT CTA TAC GGC ACC GAT GGC AAT GAT GAT ATA AAG GAT      4836
Ala Gly Leu His Leu Tyr Gly Thr Asp Gly Asn Asp Asp Ile Lys Asp
1220                1225                1230                1235

CAT GCG GAT TGG GAC AGC ATT TTG GAA GGC GGC AAA GGC AAC GAT ATT      4884
His Ala Asp Trp Asp Ser Ile Leu Glu Gly Gly Lys Gly Asn Asp Ile
                1240                1245                1250

CTA AGA GGT GGC TAC GGT GCG GAC ACC TAT ATC TTT AGC AAA GGA CAC      4932
Leu Arg Gly Gly Tyr Gly Ala Asp Thr Tyr Ile Phe Ser Lys Gly His
        1255                1260                1265

GGA CAG GAT ATC GTT TAT GAA GAT ACC AAT AAT GAT AAC CGC GCA AGA      4980
Gly Gln Asp Ile Val Tyr Glu Asp Thr Asn Asn Asp Asn Arg Ala Arg
    1270                1275                1280

GAT ATC GAC ACC TTA AAA TTT ACT GAT GTG AAT TAT GCG GAA GTG AAA      5028
Asp Ile Asp Thr Leu Lys Phe Thr Asp Val Asn Tyr Ala Glu Val Lys
1285                1290                1295

TTC CGA CGA GTA GAT AAT GAC TTA ATG TTA TTC GGT TAT CAT GAT ACG      5076
Phe Arg Arg Val Asp Asn Asp Leu Met Leu Phe Gly Tyr His Asp Thr
1300                1305                1310                1315

GAT TCG GTC ACG ATA AAA TCC TTC TAC AAC CAT GTA GAT TAT CAA TTT      5124
Asp Ser Val Thr Ile Lys Ser Phe Tyr Asn His Val Asp Tyr Gln Phe
                1320                1325                1330

GAC AAA TTG GAA TTT GCT GAC CGC AGT ATA ACT CGT GAT GAA CTA GGT      5172
Asp Lys Leu Glu Phe Ala Asp Arg Ser Ile Thr Arg Asp Glu Leu Gly
        1335                1340                1345

AAA CAA GGT ATG GCA TTA TTT GGC ACT GAC GGT GAT GAT AAT ATC AAC      5220
Lys Gln Gly Met Ala Leu Phe Gly Thr Asp Gly Asp Asp Asn Ile Asn
    1350                1355                1360

GAC TGG GGA CGT AAC TCG GTG ATT GAT GCC GGT GCG GGT AAT GAT ACG      5268
Asp Trp Gly Arg Asn Ser Val Ile Asp Ala Gly Ala Gly Asn Asp Thr
1365                1370                1375

GTT AAT GGC GGT AAT GGC GAT GAC ACC CTC ATC GGC GGC AAA GGT AAT      5316
Val Asn Gly Gly Asn Gly Asp Asp Thr Leu Ile Gly Gly Lys Gly Asn
1380                1385                1390                1395

GAT ATT CTA AGA GGT GGC TAC GGT GCG GAC ACC TAT ATC TTT AGC AAA      5364
Asp Ile Leu Arg Gly Gly Tyr Gly Ala Asp Thr Tyr Ile Phe Ser Lys
                1400                1405                1410

GGA CAC GGA CAG GAT ATC GTT TAT GAA GAT ACC AAT AAT GAT AAC CGC      5412
Gly His Gly Gln Asp Ile Val Tyr Glu Asp Thr Asn Asn Asp Asn Arg
        1415                1420                1425

GCA AGA GAT ATC GAC ACC TTA AAA TTT ACC GAT GTG AAT TAT GCG GAA      5460
Ala Arg Asp Ile Asp Thr Leu Lys Phe Thr Asp Val Asn Tyr Ala Glu
    1430                1435                1440

GTG AAA TTC CGA CGA GTA GAT AAT GAC TTA ATG TTA TTC GGT TAT CAT      5508
Val Lys Phe Arg Arg Val Asp Asn Asp Leu Met Leu Phe Gly Tyr His
1445                1450                1455

GAT ACG GAT TCG GTC ACG GTA AAA TCC TTC TAC AGC CAT GTA GAT TAT      5556
Asp Thr Asp Ser Val Thr Val Lys Ser Phe Tyr Ser His Val Asp Tyr
1460                1465                1470                1475

CAA TTT GAC AAA TTG GAG TTT GCT GAC CGC AGT ATA ACT CGC GAT GAA      5604
Gln Phe Asp Lys Leu Glu Phe Ala Asp Arg Ser Ile Thr Arg Asp Glu
                1480                1485                1490

CTG ATT AAA GCA GGG CTT CAT CTA TAC GGC ACC GAT GGC AAT GAT GAT      5652
Leu Ile Lys Ala Gly Leu His Leu Tyr Gly Thr Asp Gly Asn Asp Asp
        1495                1500                1505

ATA AAG GAT CAT GCG GAT TGG GAC AGC ATT TTG GAA GGC GGC AAA GGC      5700
Ile Lys Asp His Ala Asp Trp Asp Ser Ile Leu Glu Gly Gly Lys Gly
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          1510                1515                1520

AAC GAT ATT CTA AGA GGT GGC TAC GGT GCG GAC ACC TAT ATC TTT AGC      5748
Asn Asp Ile Leu Arg Gly Gly Tyr Gly Ala Asp Thr Tyr Ile Phe Ser
    1525                1530                1535

AAA GGA CAC GGA CAG GAT ATC GTT TAT GAA GAT ACC AAT AAT GAT AAC      5796
Lys Gly His Gly Gln Asp Ile Val Tyr Glu Asp Thr Asn Asn Asp Asn
1540                1545                1550                1555

CGA GCA AGA GAT ATC GAC ACC TTA AAA TTT ACT GAT GTG AAT TAT GCG      5844
Arg Ala Arg Asp Ile Asp Thr Leu Lys Phe Thr Asp Val Asn Tyr Ala
                1560                1565                1570

GAA GTG AAA TTC CGA CGA GTA GAT AAT GAC TTA ATG TTA TTC GGT TAT      5892
Glu Val Lys Phe Arg Arg Val Asp Asn Asp Leu Met Leu Phe Gly Tyr
            1575                1580                1585

CAT GAT ACG GAT TCG GTC ACG ATA AAA TCC TTC TAC AAC CAT GTA GAT      5940
His Asp Thr Asp Ser Val Thr Ile Lys Ser Phe Tyr Asn His Val Asp
        1590                1595                1600

TAT CAA TTT GAC AAA TTG GAA TTT GCT GAC CGC AGT ATA ACT CGT GAT      5988
Tyr Gln Phe Asp Lys Leu Glu Phe Ala Asp Arg Ser Ile Thr Arg Asp
    1605                1610                1615

GAA CTA GGT AAA CAA GGT ATG GCA TTA TTT GGC ACT GAC GGT GAT GAT      6036
Glu Leu Gly Lys Gln Gly Met Ala Leu Phe Gly Thr Asp Gly Asp Asp
1620                1625                1630                1635

AAT ATC AAC GAC TGG GGA CGT AAC TCG GTG ATT GAT GCC GGT GCG GGT      6084
Asn Ile Asn Asp Trp Gly Arg Asn Ser Val Ile Asp Ala Gly Ala Gly
                1640                1645                1650

AAT GAT ACG GTT AAT GGC GGT AAT GGC GAT GAC ACC CTC ATC GGC GGC      6132
Asn Asp Thr Val Asn Gly Gly Asn Gly Asp Asp Thr Leu Ile Gly Gly
            1655                1660                1665

AAA GGT AAT GAT ATT CTA AGA GGT GGC TAC GGT GCG GAC ACC TAT ATC      6180
Lys Gly Asn Asp Ile Leu Arg Gly Gly Tyr Gly Ala Asp Thr Tyr Ile
        1670                1675                1680

TTT AGC AAA GGA CAC GGA CAG GAT ATC GTT TAT GAA GAT ACC AAT AAT      6228
Phe Ser Lys Gly His Gly Gln Asp Ile Val Tyr Glu Asp Thr Asn Asn
    1685                1690                1695

GAT AAC CGC GCA AGA GAT ATC GAC ACC TTA AAA TTT ACT GAT ATT AAT      6276
Asp Asn Arg Ala Arg Asp Ile Asp Thr Leu Lys Phe Thr Asp Ile Asn
1700                1705                1710                1715

TTA TCC GAA CTT TGG TTT AGC CGA GAA AAT AAC GAT TTG ATT ATT AAA      6324
Leu Ser Glu Leu Trp Phe Ser Arg Glu Asn Asn Asp Leu Ile Ile Lys
                1720                1725                1730

TCA TTA TTA AGT GAG GAT AAA GTC ACG GTT CAA AAT TGG TAT TCA CAC      6372
Ser Leu Leu Ser Glu Asp Lys Val Thr Val Gln Asn Trp Tyr Ser His
            1735                1740                1745

CAA GAT CAT AAA ATA GAA AAT ATT CGT TTA TCG AAT GAG CAA ACG TTG      6420
Gln Asp His Lys Ile Glu Asn Ile Arg Leu Ser Asn Glu Gln Thr Leu
        1750                1755                1760

GTG AGC ACT CAG GTG GAG AAG ATG GTT GAG TCG ATG GCC GGC TTT GCT      6468
Val Ser Thr Gln Val Glu Lys Met Val Glu Ser Met Ala Gly Phe Ala
    1765                1770                1775

CAG AAG CAC GGA GGA GAG ATA TCT CTT GTG TCG CTT GAA GAG GTA AAA      6516
Gln Lys His Gly Gly Glu Ile Ser Leu Val Ser Leu Glu Glu Val Lys
1780                1785                1790                1795

CAA TAT ATC AAT AGC TTA ACA GCT GCT TTA TAA CATACGAAAG AAATCGGCAC    6569
Gln Tyr Ile Asn Ser Leu Thr Ala Ala Leu  *
                1800                1805

AGTTTTTTTG AACTGTGCCG ATTTGATTTT AGTGTAAGAA TATAGCCTGA TTTTAAGAAA    6629

TTTACTCTTG GCTAATAACT ATTTCCCATT TTATAAGTTA TTGACGGATG GTTTTATCAA    6689

ATATGAGATC AAATCTTATT TTAAATTCGC TTTCCATTAA GCGATAT                   6736
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(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

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Ile Asp Met Pro Pro Gly Thr Gly Asp Ile Gln Leu Thr Leu Ser Gln
 1               5                  10                  15

Gln Ile Pro Val Thr Gly Ala Val Val Val Thr Thr Pro Gln Asp Ile
            20                  25                  30

Ala Leu Leu Asp Ala Val Lys Gly Ile Ser Met Phe Gln Lys Val Ser
        35                  40                  45

Val Pro Val Leu Gly Ile Ile Glu Asn Met Ser Val His Ile Cys Gln
    50                  55                  60

Asn Cys Gly His His Glu Asp Ile Phe Gly Thr Gly Gly Ala Glu Lys
65                  70                  75                  80

Val Ala Lys Lys Tyr Gly Thr Lys Val Leu Gly Gln Met Pro Leu His
                85                  90                  95

Ile Arg Leu Arg Gln Asp Leu Asp Ala Gly Thr Pro Thr Val Val Ala
            100                 105                 110

Ala Pro Glu His Glu Thr Ser Arg Ala Tyr Ile Glu Leu Ala Ala Lys
        115                 120                 125

Val Ala Ser Glu Leu Tyr Trp Gln Gly Ser Val Ile Pro Ser Glu Ile
    130                 135                 140

Met Ile Arg Glu Val Lys *
145                 150
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(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1806 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

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Met Thr Lys Leu Thr Met Gln Asp Val Thr Asn Leu Tyr Leu Tyr Lys
 1               5                  10                  15

Thr Lys Thr Leu Pro Lys Asp Arg Leu Asp Asp Ser Leu Ile Ser Glu
            20                  25                  30

Ile Gly Lys Gly Asp Asp Asp Ile Asp Arg Lys Glu Phe Met Val Gly
        35                  40                  45

Pro Gly Arg Phe Val Thr Ala Asp Asn Phe Ser Val Val Arg Asp Phe
    50                  55                  60

Phe Asn Ala Gly Lys Ser Arg Ile Ile Ala Pro Gln Val Pro Pro Ile
65                  70                  75                  80

Arg Ser Gln Gln Glu Lys Ile Leu Val Gly Leu Lys Pro Gly Lys Tyr
                85                  90                  95

Ser Lys Ala Gln Ile Leu Glu Met Leu Gly Tyr Thr Lys Gly Gly Glu
            100                 105                 110

Val Val Asn Gly Met Phe Ala Gly Glu Val Gln Thr Leu Gly Phe Tyr
        115                 120                 125

Asp Asp Gly Lys Gly Asp Leu Leu Glu Arg Ala Tyr Ile Trp Asn Thr
    130                 135                 140

Thr Gly Phe Lys Met Ser Asp Asn Ala Phe Phe Val Ile Glu Glu Ser
145                 150                 155                 160

Gly Lys Arg Tyr Ile Glu Asn Phe Gly Ile Glu Pro Leu Gly Lys Gln
                165                 170                 175

Glu Asp Phe Asp Phe Val Gly Gly Phe Trp Ser Asn Leu Val Asn Arg
            180                 185                 190

Gly Leu Glu Ser Ile Ile Asp Pro Ser Gly Ile Gly Gly Thr Val Asn
        195                 200                 205
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Leu Asn Phe Thr Gly Glu Val Glu Thr Tyr Thr Leu Asp Glu Thr Arg
210 215 220

Phe Lys Ala Glu Ala Ala Lys Lys Ser His Trp Ser Leu Val Asn Ala
225 230 235 240

Ala Lys Val Tyr Gly Gly Leu Asp Gln Ile Ile Lys Lys Leu Trp Asp
245 250 255

Ser Gly Ser Ile Lys His Leu Tyr Gln Asp Lys Asp Thr Gly Lys Leu
260 265 270

Lys Pro Ile Ile Tyr Gly Thr Ala Gly Asn Asp Ser Lys Ile Glu Gly
275 280 285

Thr Lys Ile Thr Arg Arg Ile Ala Gly Lys Glu Val Thr Leu Asp Ile
290 295 300

Ala Asn Gln Lys Ile Glu Lys Gly Val Leu Glu Lys Leu Gly Leu Ser
305 310 315 320

Val Ser Gly Ser Asp Ile Ile Lys Leu Leu Phe Gly Ala Leu Thr Pro
325 330 335

Thr Leu Asn Arg Met Leu Leu Ser Gln Leu Ile Gln Ser Phe Ser Asp
340 345 350

Ser Leu Ala Lys Leu Asp Asn Pro Leu Ala Pro Tyr Thr Lys Asn Gly
355 360 365

Val Val Tyr Val Thr Gly Lys Gly Asn Asp Val Leu Lys Gly Thr Glu
370 375 380

His Glu Asp Leu Phe Leu Gly Gly Glu Gly Asn Asp Thr Tyr Tyr Ala
385 390 395 400

Arg Val Gly Asp Thr Ile Glu Asp Ala Asp Gly Lys Gly Lys Val Tyr
405 410 415

Phe Val Arg Glu Lys Gly Val Pro Lys Ala Asp Pro Lys Arg Val Glu
420 425 430

Phe Ser Glu Tyr Ile Thr Lys Glu Glu Ile Lys Glu Val Glu Lys Gly
435 440 445

Leu Leu Thr Tyr Ala Val Leu Glu Asn Tyr Asn Trp Glu Glu Lys Thr
450 455 460

Ala Thr Phe Ala His Ala Thr Met Leu Asn Glu Leu Phe Thr Asp Tyr
465 470 475 480

Thr Asn Tyr Arg Tyr Glu Val Lys Gly Leu Lys Leu Pro Ala Val Lys
485 490 495

Lys Leu Lys Ser Pro Leu Val Glu Phe Thr Ala Asp Leu Leu Thr Val
500 505 510

Thr Pro Ile Asp Glu Asn Gly Lys Ala Leu Ser Glu Lys Ser Ile Thr
515 520 525

Val Lys Asn Phe Lys Asn Gly Asp Leu Gly Ile Arg Leu Leu Asp Pro
530 535 540

Asn Ser Tyr Tyr Tyr Phe Leu Glu Gly Gln Asp Thr Gly Phe Tyr Gly
545 550 555 560

Pro Ala Phe Tyr Ile Glu Arg Lys Asn Gly Gly Gly Ala Lys Asn Asn
565 570 575

Ser Ser Gly Ala Gly Asn Ser Lys Asp Trp Gly Gly Asn Gly His Gly
580 585 590

Asn His Arg Asn Asn Ala Ser Asp Leu Asn Lys Pro Asp Gly Asn Asn
595 600 605

Gly Asn Asn Gln Asn Asn Gly Ser Asn Gln Asp Asn His Ser Asp Val
610 615 620

Asn Ala Pro Asn Asn Pro Gly Arg Asn Tyr Asp Ile Tyr Asp Pro Leu
625 630 635 640

Ala Leu Asp Leu Asp Gly Asp Gly Leu Glu Thr Val Ser Met Asn Gly
645 650 655

Arg Gln Gly Ala Leu Phe Asp His Glu Gly Lys Gly Ile Arg Thr Ala

660 665 670

Thr Gly Trp Leu Ala Ala Asp Asp Gly Phe Leu Val Leu Asp Arg Asn
675 680 685

Gln Asp Gly Ile Ile Asn Asp Ile Ser Glu Leu Phe Ser Asn Lys Asn
690 695 700

Gln Leu Ser Asp Gly Ser Ile Ser Ala His Gly Phe Ala Thr Leu Ala
705 710 715 720

Asp Leu Asp Thr Asn Gln Asp Gln Arg Ile Asp Gln Asn Asp Lys Leu
725 730 735

Phe Ser Lys Leu Gln Ile Trp Arg Asp Leu Asn Gln Asn Gly Phe Ser
740 745 750

Glu Ala Asn Glu Leu Phe Ser Leu Glu Ser Leu Asn Ile Lys Ser Leu
755 760 765

His Thr Ala Tyr Glu Glu Arg Asn Asp Phe Leu Ala Gly Asn Asn Ile
770 775 780

Leu Ala Gln Leu Gly Lys Tyr Glu Lys Thr Asp Gly Thr Phe Ala Gln
785 790 795 800

Met Gly Asp Leu Asn Phe Ser Phe Asn Pro Phe Tyr Ser Arg Phe Thr
805 810 815

Glu Ala Leu Asn Leu Thr Glu Gln Gln Arg Arg Thr Ile Asn Leu Thr
820 825 830

Gly Thr Gly Arg Val Arg Asp Leu Arg Glu Ala Ala Ala Leu Ser Glu
835 840 845

Glu Leu Ala Ala Leu Leu Gln Gln Tyr Thr Lys Ala Ser Asp Phe Gln
850 855 860

Ala Gln Arg Glu Leu Leu Pro Ala Ile Leu Asp Lys Trp Ala Ala Thr
865 870 875 880

Asp Leu Gln Tyr Gln His Tyr Asp Lys Thr Leu Leu Lys Thr Val Glu
885 890 895

Ser Thr Asp Ser Ser Ala Ser Val Val Arg Val Thr Pro Ser Gln Leu
900 905 910

Ser Ser Ile Arg Asn Ala Lys His Asp Pro Thr Val Met Gln Asn Phe
915 920 925

Glu Gln Ser Lys Ala Lys Ile Ala Thr Leu Asn Ser Leu Tyr Gly Leu
930 935 940

Asn Ile Asp Gln Leu Tyr Tyr Thr Thr Asp Lys Asp Ile Arg Tyr Ile
945 950 955 960

Thr Asp Lys Val Asn Asn Met Tyr Gln Thr Thr Val Glu Leu Ala Tyr
965 970 975

Arg Ser Leu Leu Leu Gln Thr Arg Leu Lys Lys Tyr Val Tyr Ser Val
980 985 990

Asn Ala Lys Gln Phe Glu Gly Lys Trp Val Thr Asp Tyr Ser Arg Thr
995 1000 1005

Glu Ala Leu Phe Asn Ser Thr Phe Lys Gln Ser Pro Glu Asn Ala Leu
1010 1015 1020

Tyr Asp Leu Ser Glu Tyr Leu Ser Phe Phe Asn Asp Pro Thr Glu Trp
1025 1030 1035 1040

Lys Glu Gly Leu Leu Leu Leu Ser Arg Tyr Ile Asp Tyr Ala Lys Ala
1045 1050 1055

Gln Gly Phe Tyr Glu Asn Trp Ala Ala Thr Ser Asn Leu Thr Ile Ala
1060 1065 1070

Arg Leu Arg Glu Ala Gly Val Ile Phe Ala Glu Ser Thr Asp Leu Lys
1075 1080 1085

Gly Asp Glu Lys Asn Asn Ile Leu Leu Gly Ser Gln Lys Asp Asn Asn
1090 1095 1100

Leu Ser Gly Ser Ala Gly Asp Asp Leu Leu Ile Gly Gly Glu Gly Asn
1105 1110 1115 1120

Asp Thr Leu Lys Gly Ser Tyr Gly Ala Asp Thr Tyr Ile Phe Ser Lys
1125 1130 1135

Gly His Gly Gln Asp Ile Val Tyr Glu Asp Thr Asn Asn Asp Asn Arg
1140 1145 1150

Ala Arg Asp Ile Asp Thr Leu Lys Phe Thr Asp Val Asn Tyr Ala Glu
1155 1160 1165

Val Lys Phe Arg Arg Val Asp Asn Asp Leu Met Leu Phe Gly Tyr His
1170 1175 1180

Asp Thr Asp Ser Val Thr Val Lys Ser Phe Tyr Ser His Val Asp Tyr
1185 1190 1195 1200

Gln Phe Asp Lys Leu Glu Phe Ala Asp Arg Ser Ile Thr Arg Asp Glu
1205 1210 1215

Leu Ile Lys Ala Gly Leu His Leu Tyr Gly Thr Asp Gly Asn Asp Asp
1220 1225 1230

Ile Lys Asp His Ala Asp Trp Asp Ser Ile Leu Glu Gly Gly Lys Gly
1235 1240 1245

Asn Asp Ile Leu Arg Gly Gly Tyr Gly Ala Asp Thr Tyr Ile Phe Ser
1250 1255 1260

Lys Gly His Gly Gln Asp Ile Val Tyr Glu Asp Thr Asn Asn Asp Asn
1265 1270 1275 1280

Arg Ala Arg Asp Ile Asp Thr Leu Lys Phe Thr Asp Val Asn Tyr Ala
1285 1290 1295

Glu Val Lys Phe Arg Arg Val Asp Asn Asp Leu Met Leu Phe Gly Tyr
1300 1305 1310

His Asp Thr Asp Ser Val Thr Ile Lys Ser Phe Tyr Asn His Val Asp
1315 1320 1325

Tyr Gln Phe Asp Lys Leu Glu Phe Ala Asp Arg Ser Ile Thr Arg Asp
1330 1335 1340

Glu Leu Gly Lys Gln Gly Met Ala Leu Phe Gly Thr Asp Gly Asp Asp
1345 1350 1355 1360

Asn Ile Asn Asp Trp Gly Arg Asn Ser Val Ile Asp Ala Gly Ala Gly
1365 1370 1375

Asn Asp Thr Val Asn Gly Gly Asn Gly Asp Asp Thr Leu Ile Gly Gly
1380 1385 1390

Lys Gly Asn Asp Ile Leu Arg Gly Gly Tyr Gly Ala Asp Thr Tyr Ile
1395 1400 1405

Phe Ser Lys Gly His Gly Gln Asp Ile Val Tyr Glu Asp Thr Asn Asn
1410 1415 1420

Asp Asn Arg Ala Arg Asp Ile Asp Thr Leu Lys Phe Thr Asp Val Asn
1425 1430 1435 1440

Tyr Ala Glu Val Lys Phe Arg Arg Val Asp Asn Asp Leu Met Leu Phe
1445 1450 1455

Gly Tyr His Asp Thr Asp Ser Val Thr Val Lys Ser Phe Tyr Ser His
1460 1465 1470

Val Asp Tyr Gln Phe Asp Lys Leu Glu Phe Ala Asp Arg Ser Ile Thr
1475 1480 1485

Arg Asp Glu Leu Ile Lys Ala Gly Leu His Leu Tyr Gly Thr Asp Gly
1490 1495 1500

Asn Asp Asp Ile Lys Asp His Ala Asp Trp Asp Ser Ile Leu Glu Gly
1505 1510 1515 1520

Gly Lys Gly Asn Asp Ile Leu Arg Gly Gly Tyr Gly Ala Asp Thr Tyr
1525 1530 1535

Ile Phe Ser Lys Gly His Gly Gln Asp Ile Val Tyr Glu Asp Thr Asn
1540 1545 1550

Asn Asp Asn Arg Ala Arg Asp Ile Asp Thr Leu Lys Phe Thr Asp Val
1555 1560 1565

Asn Tyr Ala Glu Val Lys Phe Arg Arg Val Asp Asn Asp Leu Met Leu

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    1570                1575                1580

Phe Gly Tyr His Asp Thr Asp Ser Val Thr Ile Lys Ser Phe Tyr Asn
1585                1590                1595                1600

His Val Asp Tyr Gln Phe Asp Lys Leu Glu Phe Ala Asp Arg Ser Ile
                1605                1610                1615

Thr Arg Asp Glu Leu Gly Lys Gln Gly Met Ala Leu Phe Gly Thr Asp
            1620                1625                1630

Gly Asp Asp Asn Ile Asn Asp Trp Gly Arg Asn Ser Val Ile Asp Ala
        1635                1640                1645

Gly Ala Gly Asn Asp Thr Val Asn Gly Gly Asn Gly Asp Asp Thr Leu
    1650                1655                1660

Ile Gly Gly Lys Gly Asn Asp Ile Leu Arg Gly Gly Tyr Gly Ala Asp
1665                1670                1675                1680

Thr Tyr Ile Phe Ser Lys Gly His Gly Gln Asp Ile Val Tyr Glu Asp
                1685                1690                1695

Thr Asn Asn Asp Asn Arg Ala Arg Asp Ile Asp Thr Leu Lys Phe Thr
            1700                1705                1710

Asp Ile Asn Leu Ser Glu Leu Trp Phe Ser Arg Glu Asn Asn Asp Leu
        1715                1720                1725

Ile Ile Lys Ser Leu Leu Ser Glu Asp Lys Val Thr Val Gln Asn Trp
    1730                1735                1740

Tyr Ser His Gln Asp His Lys Ile Glu Asn Ile Arg Leu Ser Asn Glu
1745                1750                1755                1760

Gln Thr Leu Val Ser Thr Gln Val Glu Lys Met Val Glu Ser Met Ala
                1765                1770                1775

Gly Phe Ala Gln Lys His Gly Gly Glu Ile Ser Leu Val Ser Leu Glu
            1780                1785                1790

Glu Val Lys Gln Tyr Ile Asn Ser Leu Thr Ala Ala Leu  *
        1795                1800                1805
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Claims

1. Live attenuated bacterium of the species *Actinobacillus pleuropneumoniae,* characterised in that said bacterium produces no functional ApxIV toxin.

2. Live attenuated bacterium according to claim 1, characterised in that the gene encoding the ApxIV toxin comprises a mutation.

3. Live attenuated bacterium according to claim 2, characterised in that said mutation is an insertion and/or deletion.

4. Live attenuated bacterium according to claim 3, characterised in that the insertion comprises a heterologous gene.

5. Live attenuated bacterium according to claim 4, characterised in that said heterologous gene encodes one or more antigens selected from the group consisting of Porcine Reproductive Respiratory Syndrome (PRRS) virus, Pseudorabies virus, Porcine Influenza virus, Porcine Parvovirus, Transmissible Gastroenteritis virus, rotavirus, *Escherichia coli, Erysipelothrix rhusiopathiae, Pasteurella multocida, Bordetella bronchiseptica, Haemophilus parasuis* and *Streptococcus suis.*

6. Live attenuated bacterium according to claim 4 or 5, characterised in that said heterologous gene is functionally linked to the promotor region of the *apxIV* gene.

7. Nucleotide sequence harbouring the promotor controling the expression of the *apxIV* gene.

8. Nucleotide sequence according to claim 7, characterised in that it comprises the DNA fragment from position 451 to 1132 of SEQ ID NO: 5 or a subfragment thereof still having promotor activity.

9. Nucleotide sequence according to claim 7, characterised in that it comprises the DNA fragment from position 617 to 641 of SEQ ID NO: 5.

10. Subunit vaccine for the protection of animals against infection with a bacterium of the species *Actinobacillus pleuropneumoniae,* characterised in that said vaccine comprises purified ApxIV toxin and a pharmaceutically acceptable carrier.

11. Live attenuated vaccine for the protection of animals against infection with a bacterium of the species *Actinobacillus pleuropneumoniae,* characterised in that said vaccine comprises a live attenuated bacterium according to claims 1-6 and a pharmaceutically acceptable carrier.

12. Vaccine according to claim 10 or 11, characterised in that it comprises an adjuvant.

13. Vaccine according to claim 10-12, characterised in that the vaccine is in a freeze-dried form.

14. Vaccine according to claims 10-13, characterised in that it additionally comprises one or more antigens from pig-pathogenic micro-organisms or viruses.

15. Vaccine according to claim 14, characterised in that it additionally comprises one or more antigens selected from the group consisting of Porcine Reproductive Respiratory Syndrome (PRRS) virus, Pseudorabies virus, Porcine Influenza virus, Porcine Parvovirus, Transmissible Gastroenteritis virus, rotavirus, *Escherichia coli, Erysipelothrix rhusiopathiae, Pasteurella multocida, Bordetella bronchiseptica, Haemophilus parasuis* and *Streptococcus suis.*

16. Method for the protection of a susceptible animal against *Actinobacillus pleuropneumoniae* infection, said method comprising administering a vaccine according to claims 10-15.

17. Method for the preparation of a live attenuated bacterium of the species *Actinobacillus pleuropneumoniae* producing no functional ApxIV toxin, characterised in that said method comprises the introduction of a mutation in the gene encoding the apxIV protein.

18. Method according to claim 17, characterised in that said mutation is obtained by introducing a deletion

19. Method for the preparation of a live attenuated vaccine according to claims 11-15, said method comprising admixing bacteria according to claims 1-6 with a pharmaceutically acceptable carrier.

20. Method for the preparation of a vaccine according to claim 10, said method comprising admixing purified ApxIV toxin with a pharmaceutically acceptable carrier.

21. Diagnostic test for the discrimination between sera from pigs infected with *Actinobacillus pleuropneumoniae* field strains and from pigs vaccinated with a vaccine comprising live attenuated vaccine *Actinobacillus pleuropneumoniae* strains according to claim 1, said test being characterised in that the test comprises purified ApxIV toxin.

22. Diagnostic test for distinguishing *Actinobacillus pleuropneumoniae* infection in pigs from *A. suis* infection in pigs, characterised in that said test comprises purified ApxIV toxin.

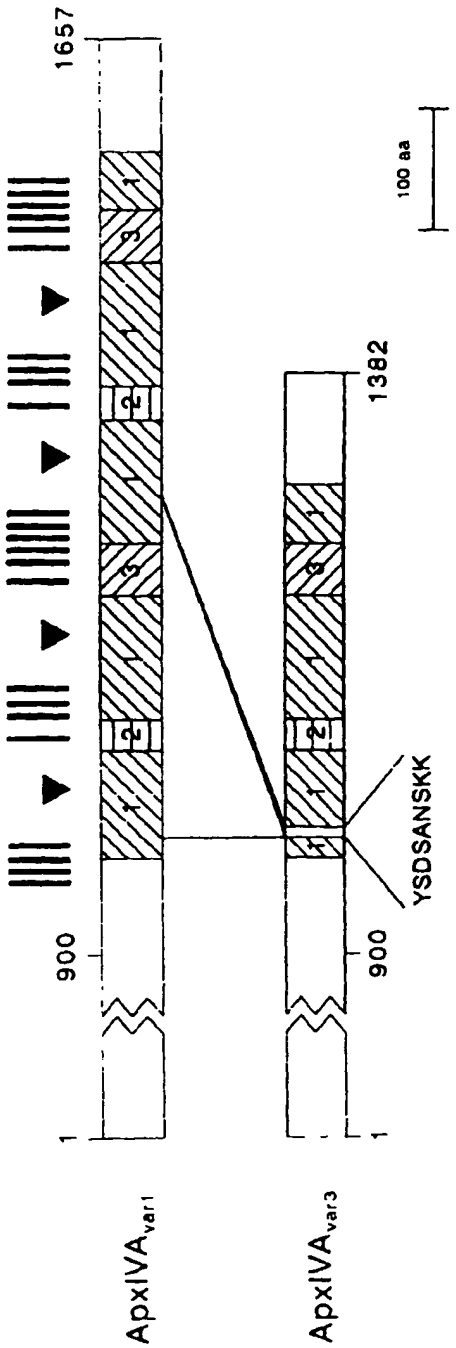
1657
900
1
100 aa
1382
900
1
YSDSANSKK
ApxIVA$_{var1}$
ApxIVA$_{var3}$

Figure 1

A

```
                1                                                          60
REP1var1:A      .......... .YGADTYIFS KGHGQDIVYE DTNNDNRARD IDTLKFTDVN YAEVKFRRVD
REP1var1:B      GGKGNDILRG GYGADTYIFS KGHGQDIVYE DTNNDNRARD IDTLKFTDVN YAEVKFRRVD
REP1var1:C      GGKGNDILRG GYGADTYIFS KGHGQDIVYE DTNNDNRARD IDTLKFTDVN YAEVKFRRVD
REP1var1:D      GGKGNDILRG GYGADTYIFS KGHGQDIVYE DTNNDNRARD IDTLKFTDVN YAEVKFRRVD
REP1var1:E      GGKGNDILRG GYGADTYIFS KGHGQDIVYE DTNNDNRARD IDTLKFTD.. ..........
REP1var1:A      .......... .YGADTYIFS KGHGQDVIYE .......... .......... ..........
REP1var1:B      .......... .......... .......... .........D IDTLKFTDVN YAEVKFRRVD
REP1var1:C      GGKGNDILRG GYGADTYIFS KGHGQDIVYE DTNNDNRARD IDTLKFTDVN YAEVKFRRVD
REP1var1:D      GGKGNDILRG GYGADTYIFS KGHGQDIVYE DTNNDNRARD IDTLKFTD.. ..........

                61                                                        102
REP1var1:A      NDLMLFGYHD TDSVTVKSFY SHVDYQFDKL EFADRSITRD EL
REP1var1:B      NDLMLFGYHD TDSVTIKSFY NHVDYQFDKL EFADRSITRD EL
REP1var1:C      NDLMLFGYHD TDSVTVKSFY SHVDYQFDKL EFADRSITRD EL
REP1var1:D      NDLMLFGYHD TDSVTIKSFY NHVDYQFDKL EFADRSITRD EL
REP1var1:E      .......... .......... .......... .......... ..
REP1var1:A      .......... .......... .......... .......... ..
REP1var1:B      NDLMLFGYHD TDSVTVKSFY SHVDYQFDKL EFADRSITRD EL
REP1var1:C      NDLMLFGYHD TDSVTIKSFY NHVDYQCDKL DFADRSITRD EL
REP1var1:D      .......... .......... .......... .......... ..
```

B

```
                1                    27
REP2var1:A      IKAGLHLYGT DGNDDIKDHA DWDSILE
REP2var1:B      IKAGLHLYGT DGNDDIKDHA DWDSILE
REP2var1:A      IKAGLHLYGT DGNDDIKDHA DWDSIVE
```

C

```
                1                                                      44
REP3var1:A      GKQGMALFGT DGDDNINDWG RNSVIDAGAG NDTVNGGNGD DTLI
REP3var1:B      GKQGMALFGT DGDDNINDWG RNSVIDAGAG NDTVNGGNGD DTLI
REP3var1:A      GKQGMALFGT DGDDNINDWG RNSVIDAGAG NDTVNGGNGD DTLI
```

Figure 2

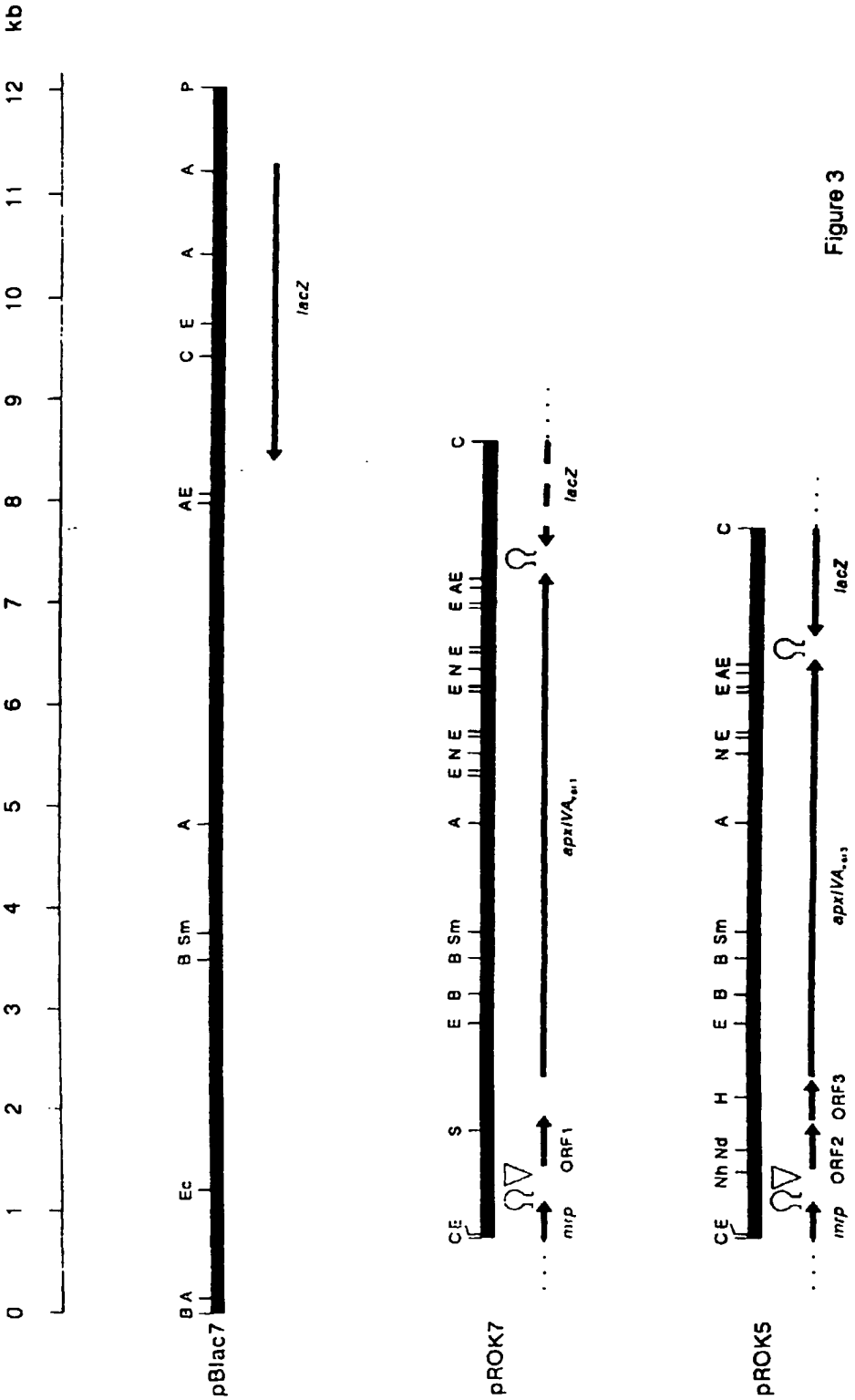
kb
0 1 2 3 4 5 6 7 8 9 10 11 12
pBlac7
lacZ
pROK7
mrp
ORF1
apxIVA
pROK5
ORF2
ORF3

Figure 3

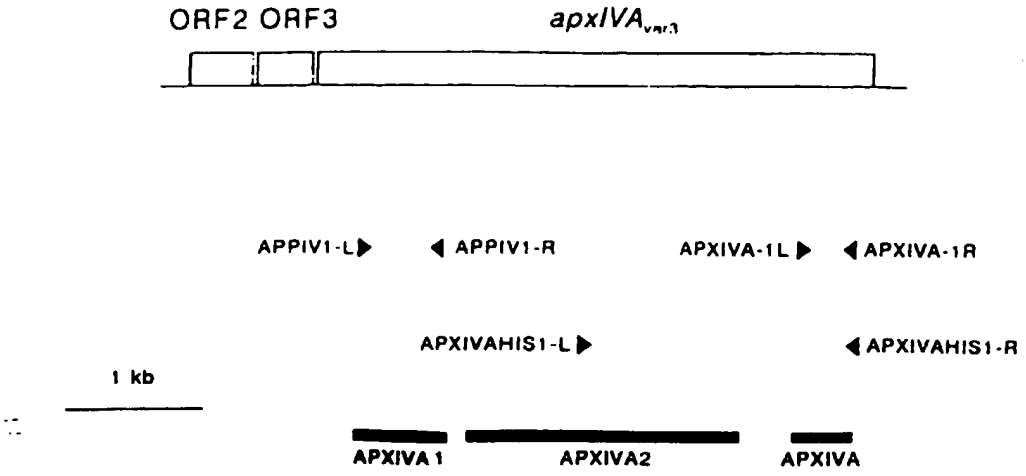
ORF2 ORF3
apxIVA
APPIV1-L
APPIV1-R
APXIVA-1L
APXIVA-1R
APXIVAHIS1-L
APXIVAHIS1-R
1 kb
APXIVA 1
APXIVA2
APXIVA

Figure 4

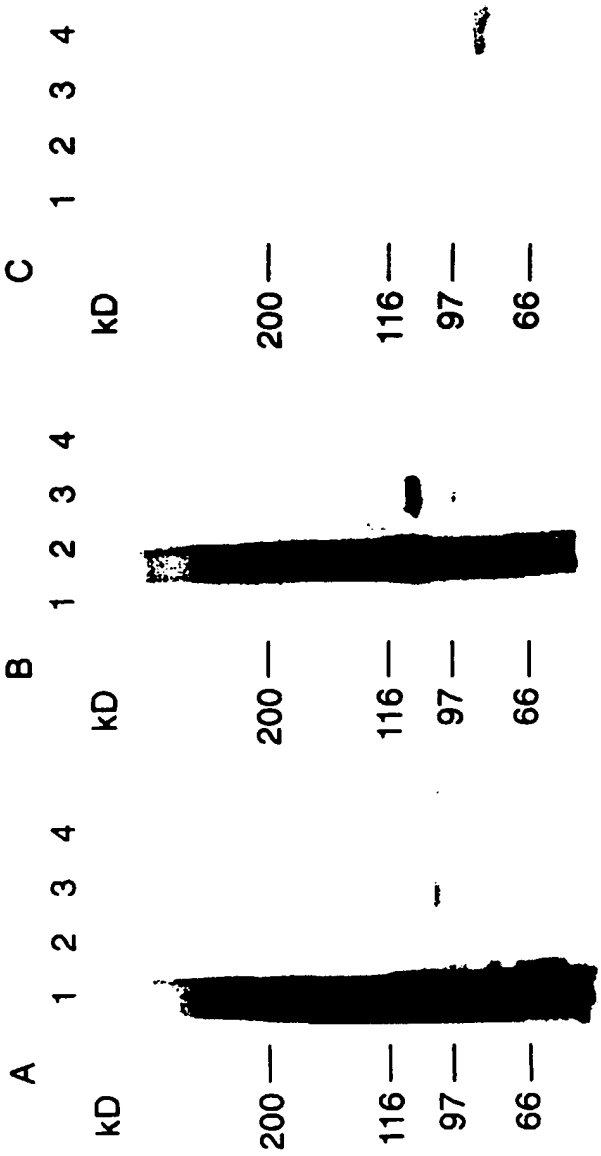
A
1 2 3 4
kD
200
116
97
66
B
1 2 3 4
kD
200
116
97
66
C
1 2 3 4
kD
200
116
97
66

Figure 5

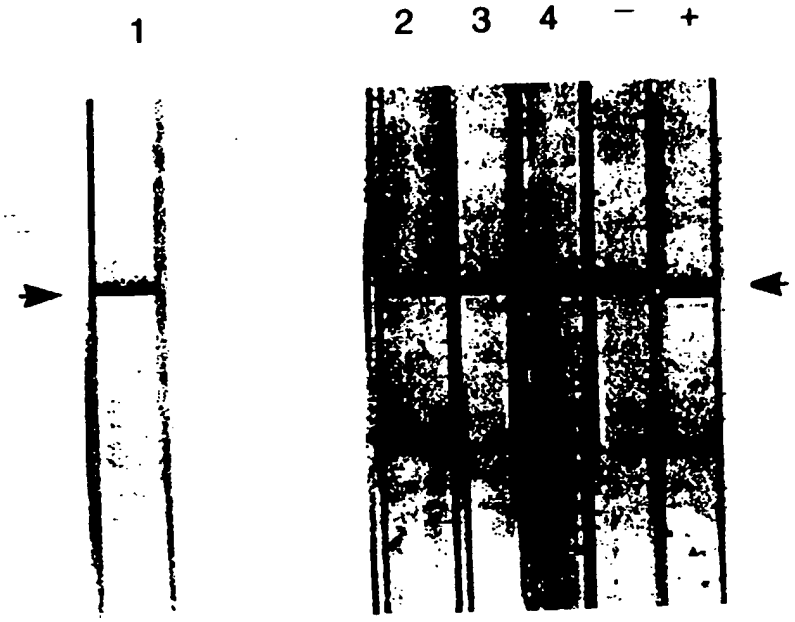

Figure 6

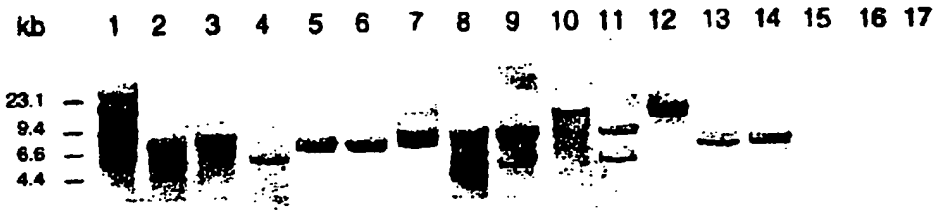

Figure 7

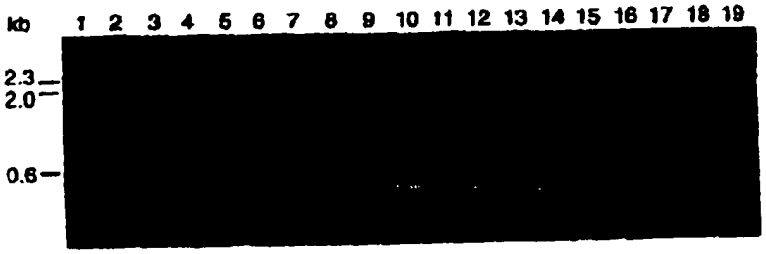

Figure 8